

- u89336exon#54_51-
 369:not_in_gb_record_unknown_gene_extracted_fromhla_iii_region_containing_notch4_g
 u89336exon#65_12-282:in_reversesequence,_54136-
 54166:not_in_gb_record_unknown_gene_extracted_fromhl
- 5** u92436_2591-3077,mutated_in_multiple_advanced_cancers_protein_(mmac1)_mrna,_complete_cds.
 x03072cds_765-1089:in_reversesequence,_3505-3649,int-1_mammary_oncogene_
 x04707cds_815-1343:in_reversesequence,_1649-1673,c-erb-a_mrna_for_thyroid_hormone_receptor
 all_x07203_1419-1576,mrna_for_cd20_receptor_(s7)_
 all_x16866_688-1280,mrna_for_cytochrome_p-450iid_(clone_pmp33)_
- 10** all_x51823_2-51,mrna_for_b-
 subunit_of_coagulation_factor_xiii_(fxiiib)_(partial)/gb=x51823_/ntype=rn
 x52008cds_899-1325:in_reversesequence,_1748-1814,alpha-
 2_strychnine_binding_subunit_of_inhibitory_g1
 x58431mrna#1_1781-2299,_hox_2.2_gene_extracted_fromhox2.2_gene_for_a_homeobox_protein_
- 15** x61072mrna_43-325,mrna_for_t_cell_receptor,_clone_igra17.
 all_x62466_25-410,mrna_for_campath-1_(cdw52)_antigen_
 all_x68314_466-923,mrna_for_glutathione_peroxidase-gi
 x80923mrna_31-361,nov_gene/gb=x80923_/ntype=dna_/annot=mrna
 all_x89059_722-1203,mrna_for_unknown_protein_expressed_in_macrophages
- 20** x90763_1272-1632,mrna_for_type_i_keratin,_hha5_
 x91103cds_587-965:in_reversesequence,_1055-1097,mrna_for_hr44_protein/gb=x91103_/ntype=rna
 all_z11737_1537-2120,mrna_for_flavin-containing_monooxygenase_4
 z15114cds_1319-1589:in_reversesequence,_1595-
 1805,mrna_for_protein_kinase_c_gamma_(partial)_
- 25** all_z48482_2998-3401,mrna_for_membrane-type_matrix_metalloproteinase_2_
 all_z80783_510-565,h2b/l_gene
 all_z83336_618-702,hh2b/d_gene.
 z83821cds#2_1428-1668:in_reversesequence,_39964-
 40156,dna_sequence_from_pac_296k21_on_chromosome_x_c
- 30** Metagene 433
- af000573mrna_1162-1666,homogentisate_1,2-dioxygenase_gene,_complete_cds.
 d45399mrna_155-
- 35** 629,adult_neural_retina_mrna_forcone_cgmp_phosphodiesterase_gamma_subunit,_complete_c
 hg4557-ht4962_r_at_hg4557-ht4962_small_nuclear_ribonucleoprotein_u1,_lsnrp_
 k03189cds_2-404,chorionic_gonadotropin_beta_subunit_gene_
 all_143579_398-
 428,(clone_110298)_mrna/gb=143579_/ntype=rna,(clone_110298)_mrna/gb=143579_/ntype=rna

- all_m17236_1896-2224,mhc_ii_hla-dq-alpha_gene_(dr4,w6),mhc_ii_hla-dq-alpha_gene_(dr4,w6)
 all_m17236_1896-2224,mhc_ii_hla-dq-alpha_gene_(dr4,w6),mhc_ii_hla-dq-alpha_gene_(dr4,w6)
 m60828_3252-3720,keratinocyte_growth_factor_mrna,_complete_cds_
 s76853_1683-2244,_cerebrin-
- 5** 50=cerebrospinal_fluid_protein_[human,_cerebral_brain,_mrna,_2295_nt]
 u43189_2384-2942,ets_transcription_factors_nerf-1a_and_nerf-1b_(nerf-1a,b)_mrna,_complete_cds
 v00571mrna_714-1218,gene_encoding_prepro_form_of_corticotropin_releasing_factor_
 all_x04571_4306-4835,mrna_for_kidney_epidermal_growth_factor_(egf)_precursor_
 x61755mrna_1020-1562,hox3d_gene_for_homeoprotein_hox3d
- 10** all_x66403_1856-2301,mrna_for_acetylcholine_receptor_(epsilon_subunit)_
 x80695cds_938-1250:in_reversesequence,_1298-1496,oxalhs_mrna_
 all_z22535_2433-2932,alk-3_mrna
 z50781cds_100-205:in_reversesequence,_346-394,mrna_for_leucine_zipper_protein_
- 15** Metagene 320
- d17400_196-622,mrna_for_6-pyruvoyl-tetrahydropterin_synthase,_complete_cds_
 d38498_37-604,pms5_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-
 terminal_region)
- 20** hg3991-ht4261_r_at_hg3991-ht4261_cpg-enriched_dna,_clone_e18_
 j05500mrna#1_6200-6740,beta-spectrin_(sptb)_mrna,_complete_cds_
 l13689mrna_2674-3076,prot-oncogene_(bmi-1)_mrna,_complete_cds
 u18291_1439-1973,cdc16hs_mrna,_complete_cds
 u22662_1017-1473,nuclear_orphan_receptor_lxr-alpha_mrna,_complete_cds
- 25** u35100_330-915,complexin_ii_mrna,_complete_cds.
 x05855cds_12-65:not_in_gb_record,histone_h3.3_gene_exon_2,histone_h3.3_gene_exon_2_
 all_x63597_5486-5979,si_mrna_for_sucrase-isomaltase
 all_x68486_2465-2934,mrna_for_a2a_adenosine_receptor_
 all_z23091_6853-7358,gpv_gene_encoding_platelet_glycoprotein_v_precursor
- 30** Metagene 246
- hg2380-ht2476_s_at_hg2380-ht2476_adp-ribosylarginine_hydrolase_
 m35252_602-998,co-029
- 35** u59325_2353-2815,cadherin-14_mrna,_complete_cds
 y12812cds_486-768:in_reversesequence,_914-1130,rfxap_mrna_
 Metagene 46

- af000424_214-610,lst1_mrna,_clst1/c_splice_variant,_complete_cds
d30036_1743-2283,mrna_for_phosphatidylinositol_transfer_protein_(pi-tpalpha),_complete_cds_
d64109_642-1152,mrna_for_tob_family,_complete_cds
111672_3266-
- 5** 3562,kruppel_related_zinc_finger_protein_(htf10)_mrna,_complete_cds,kruppel_related_zinc
115326_2760-3323,endoperoxide_synthase_type_ii_mrna,_complete_cds
m27543mrna_2548-3070,guanine_nucleotide-
binding_protein_(gi)_alpha_subunit_mrna,_complete_cds
m29335_2-180,mhc_ii_do-alpha_mrna,_partial_cds,mhc_ii_do-alpha_mrna,_partial_cds
- 10** m95178_2567-2996,non-muscle_alpha-actinin_mrna,_complete_cds_
u37248_848-1304,alpha-mannosidase_(6a8)_mrna,_complete_cds_
u42387_1180-1642,pancreatic_polypeptide_receptor_mrna,_complete_cds
u49957_5044-5581,lim_protein_(lpp)_mrna,_partial_cds_
u66661_2656-3082,gaba-a_receptor_epsilon_subunit_mrna,_complete_cds
- 15** u77665_393-873,mnasep_protein_p30_(rpp30)_mrna,_complete_cds.
u78524_1571-1967,gu_binding_protein_mrna,_partial_cds
u90904_1102-1342,clone_23773_mrna_sequence_
x01630cds_883-1213:in_reversesequence,_1312-1468,mrna_for_argininosuccinate_synthetase
x04143cds_49-265:in_reversesequence,_1430-1592,gene_for_bone_gla_protein_(bglp)
- 20** all_x16832_840-1381,mrna_for_cathepsin_h_(ec_3.4.22.16)
all_x54936_1140-1627,mrna_for_placenta_growth_factor_(plgf)
all_x70683_2322-2752,mrna_for_sox-4_protein
all_x85545_1122-1591,mrna_for_protein_kinase,_pkx1_
all_x90392_2058-2545,mrna_for_dnase_x_gene_
- 25** z32765exon_79-159,cd36_gene_exon/gb=z32765_/ntype=dna_/annot=exon
- Metagene 318
- 30** hg3111-ht3287_at_hg3111-ht3287_autoantigen_
m57230_2652-3000,membrane_glycoprotein_gp130_mrna,_complete_cds
all_x68487_1174-1667,mrna_for_a2b_adenosine_receptor_
all_x89430_1828-2333,mrna_for_methyl_cpg_binding_protein_2_
z18951cds_311-509:in_reversesequence,_627-813,mrna_for_caveolin_
- 35** Metagene 424
- hg311-ht311_at_hg311-ht311_ribosomal_protein_l30_
m26167mrna_385-730,platelet_factorvaration(pf4var1)_gene,_complete_cds

- m28219_7-
 253,low_density_lipoprotein_receptor_(f1mutant_causing_familial_hypercholesterolemia)_mrna,
 m57892mrna_775-1267,carbonic_anhydrase_isozyme_vi_(ca6)_mrna,_complete_cds_
 u09303_2354-2870,t_cell_leukemia_lerk-2_(eplg2)_mrna,_complete_cds_
5 v00594mrna_15-316,mrna_for_metallothionein_from_cadmium-
 treated_cells,mrna_for_metallothionein_from_
 x59871mrna_2672-2836,tcf-1_mrna_for_t_cell_factor(splice_form_c)
 z47556mrna#2_1596-
 1866,_semenogelin_ii_gene_extracted_fromgenes_for_semenogelin_i_and_semenogelin_ii
10 Metagene 324
 d29810_835-1363,mrna_for_unknown_product,_partial_cds
 l76224_3424-3970,nmda_receptor_mrna,_complete_cds_
15 all_m24349_838-1316,parathyroid_hormone-like_protein_(plp)_gene,_exon_4,_clones_lambda-
 plpg(1,3,7-2)
 s81944_1173-1689,_gamma-
 aminobutyric_acid_type_a_receptor_alphasubunit_[human,_cerebellum,_mrna_part
 all_u03642_1060-1565,g_protein-coupled_receptor_apj_gene,_complete_cds_
20 all_u06155_512-
 660,chromosome_1q_subtelomeric_sequence_dls553/gb=u06155_/ntype=dna_/annot=cds,chromo
 u19557_998-1104,squamous_cell_carcinoma_antigen(scca2)_mrna,_complete_cds_
 u32659_1393-1825,il-17_mrna,_complete_cds
 u43519_2976-3474,dystrophin-related_protein(drp2)_mrna,_complete_cds
25 u88902_cds1_f_at_u88902_u88902,_40_in_u88902cds#1_19-247:_21_in_reversesequence,_289-
 499,_integrase_
 x80915mrna_1908-2322,gdf5_gene
 y10205mrna_146-548,mrna_for_cd88_protein/gb=y10205_/ntype=rna
30 Metagene 204
 d42040_4334-4623,mrna_for_kiaa9001_gene,_complete_cds
 u07695_3362-3770,tyrosine_kinase_(htk)_mrna,_complete_cds
 u19252_4495-5045,putative_transmembrane_protein_mrna,_complete_cds_
35 u32680_1088-1664,cln3_mrna,_complete_cds_
 u80073_1289-1655,tip_associating_protein_(tap)_mrna,_complete_cds/gb=u80073_/ntype=rna_
 x06745mrna_4850-5288,mrna_for_dna_polymerase_alpha-subunit_
 all_x52896_1629-2195,rna_for_dermal_fibroblast_elastin_
 x53742mrna_1930-2470,mrna_for_fibulin-1_b

- x54667cds_110-326,mrna_for_cystatin_s,mrna_for_cystatin_s_
 x59303cds_3274-3773,g7a_mrna_for_valyl-trna_synthetase_
 x64728cds_1694-1946:in_reversesequence,_2140-2278,chml_mrna
 x79440cds_1303-1759:in_reversesequence,_1827-1851,mrna_for_nadp+-dependent_malic_enzyme_
5 all_x97198_5010-5545,mrna_for_receptor_phosphate_pcp-2_
 all_x99975_3672-4243,mrna_for_htrr/hgcnf_protein_
 y08612cds_1849-2197:in_reversesequence,_2257-2269,mrna_for_nup88_protein
 y10514mrna_6-270,mrna_for_cd152_protein/gb=y10514_/ntype=rna_
 all_z80788_607-1040,h4/l_gene

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Metagene 101

- d13814_960-1532,mrna_for_angiotensin_ii_type_1b_receptor,_complete_cds_
 m63175_1221-1689,autocrine_motility_factor_receptor_mrna_
15 u22029_1690-2227,cytochrome_p450_(cyp2a7)_mrna,_complete_cds_
 x13930cds_1147-1454:in_reversesequence,_1650-1695,cyp2a4_mrna_for_p-450_iaa4_protein
 x63187mrna_91-511,he4_mrna_for_extracellular_proteinase_inhibitor_homologue

Metagene 177

20

- hg1148-ht1148_at_hg1148-ht1148_lipopolysaccharide-binding_protein
 hg2309-ht2405_at_hg2309-ht2405_insulin-like_growth_factor_ib_
 u70370_1511-2012,hindlimb_expressed_homeobox_protein_backfoot_(bft)_mrna,_complete_cds_
 all_x15573_2313-2800,liver-type_1-phosphofructokinase_(pfkl)_mrna,_complete_cds
25 x66365cds_543-957:in_reversesequence,_1080-
 1206,mrna_plstire_for_serine/threonine_protein_kinase
 all_x85786_1751-2262,mrna_for_dna_binding_regulatory_factor
 x86564cds_417-446:not_in_gb_record,fhr-2_gene,_exon_1_
 all_x95240_1487-2056,mrna_for_cysteine-rich_secretory_protein-3

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Metagene 52

- hg2841-ht2969_s_at_hg2841-ht2969_albumin_altsplice_3_missplicing_in_alloalbumin_venezia
 hg3417-ht3600_s_at_hg3417-ht3600_gtp_cyclohydrolase_i_altsplice_1_
35 j05008exon#5_637-1183,endothelin-1_(edn1)_gene,_complete_cds
 u44105_314-574,rab9_expressed_pseudogene_mrna,_complete_cds
 all_x04602_920-1086,mrna_for_interleukin_bsf-2_(b-cell_differentiation_factor)_

Metagene 93

- d85423_133-439,mrna_for_cdc5,_partial_cds/gb=d85423_/ntype=rna_
u23070_938-1460,putative_transmembrane_protein_(nma)_mrna,_complete_cds
all_x52001_1770-2281,endothelinmrna_
5 x83863cds_1151-1241,mrna_for_prostaglandin_e_receptor_(ep3f)_
z34822_f_at_z34822_z34822_4040_in_z34822_6145-6595,(hlcc85)_mrna_for_voltage-
dependent_l-type_ca_ch
- Metagene 421
10 hg3255-ht3432_at_hg3255-ht3432_gamma-aminobutyric_acid_(gaba)_a_receptor_betasubunit
hg4108-ht4378_at_hg4108-ht4378_olfactory_receptor_or17-24
m22490_1282-1630,bone_morphogenetic_protein-2b_(bmp-2b)_mrna_
m95925_1366-1852,leucine_zipper_on_the_d14s46e_locus_mrna,_complete_cds
15 u27333_2523-
2728,alpha_(1,3)_fucosyltransferase_(fut6)_mrna,_major_transcript_i,_complete_cds,alpha_
u35735_2115-2442,rach1_(rach1)_mrna,_complete_cds
u44799_299-860,u1-snrnp_binding_protein_homolog_mrna,_complete_cds_
20 Metagene 371
d86096_cds6_at_d86096_d86096,not_in_gb_record,_ep3-
iv_gene_extracted_fromdna_for_prostaglandin_e_rec
s62907_1577-2136,_gamma-
25 aminobutyric_acida_receptor_alphasubunit_[human,_fetal_brain,_mrna,_2189_nt]
u33920_2564-2644,clone_lambdasemaphorin_mrna,_complete_cds
u87309_4315-4843,hvps41p_(hvps41)_mrna,_complete_cds_
u96114_2964-3390,nedd-4-like_ubiquitin-protein_ligase_wwp2_mrna,_complete_cds.
all_x82018_2942-3459,mrna_for_zid_protein
30 Metagene 306
hg3238-ht4861_s_at_hg3238-ht4861_prostaglandin_ep3_receptor,_altsplice_8_
s72904_1884-
35 2322,_apk1_antigen=mab_ki_recognized_[human,_ovarian_carcinoma_cell_line_ovcar-3,_mrna,_
u45285_2099-2579,specific_116-kda_vacuolar_proton_pump_subunit_(oc-
116kda)_mrna,_complete_cds
u80017mrna#1_412-
673,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcription

x01057mrna_1492-1738,mrna_for_interleukin-2_receptor_
 x95592_558-1122,mrna_for_cld_protein_
 x97301mrna_13-148,mrna_for_ptg-11_protein/gb=x97301_/ntype=ma_

5 Metagene 479

- ab002318_6384-6786,mrna_for_kiaa0320_gene_partial_cds/gb=ab002318_/ntype=ma
 ac000099_12194-12426:in_ac000099cds_519-556:in_all_ac000099_12207_cosmid_g0771a003_
 af010193_2552-3044,mad-related_gene_smad7_(smad7)_mrna_complete_cds
- 10 d13634_1915-2419,mrna_for_kiaa0009_gene_complete_cds
 d17516_1075-1615,mrna_for_pacap_receptor_complete_cds_
 d61391_1169-1685,mrna_for_phosphoribosypyrophosphate_synthetase-
 associated_protein_39_complete_cds
 d78011_1552-2098,mrna_for_dihydropyrimidinase_complete_cds
- 15 d83920_732-1158,uterus_mrna_forficolin-1_complete_cds
 hg1723-ht1729_at_hg1723-ht1729_macrophage_scavenger_receptor_altsplice_2
 hg315-ht315_at_hg315-ht315_beta-1-glycoprotein_11_pregnancy-specific
 hg3242-ht3419_s_at_hg3242-ht3419_calcium_channel_voltage-
 gated_alpha_1e_subunit_altsplice_2
- 20 j03798_1026-1536,autoantigen_small_nuclear_ribonucleoprotein_sm-d_mrna_complete_cds_
 l01664_43-529,eosinophil_charcot-
 leyden_crystal_(clc)_protein_(lysophospholipase)_mrna_complete_cds
 l03411_798-1260,rd_protein_(rd)_mrna_complete_cds_
 all_l05512_1285-1313:not_in_gb_record,histatin(his1)_gene
- 25 l25441_1410-1890,geranylgeranyltransferase_type_i_beta-subunit_mrna_complete_cds
 l26081_1959-2487,semaphorin-iii_(hsema-i)_mrna_complete_cds
 l38929mrna_5668-6190,protein_tyrosine_phosphatase_delta_mrna_complete_cds
 l40586_1123-1255,iduronate-2-sulphatase_(ids)_mrna_complete_cds
 l41066_2321-2831,nf-at3_mrna_complete_cds
- 30 l76670_502-1071,nkat7_mrna_complete_cds
 m58297_2215-2653,zinc_finger_protein_42_(mzf-1)_mrna_complete_cds_
 m91036mrna#1_37-529_g-gamma_globin_gene_extracted_fromg-gamma_globin_and_a-
 gamma_globin_genes_comp
 m95724_2549-2939,centromere_autoantigen_c_(cenpc)_mrna_complete_cds_
- 35 s78203_2096-2660_pept_2=h+/peptide_cotransporter_[human_kidney_mrna_partial_2685_nt]
 s83365_109-343_putative_rab5-interacting_protein_{clone_11-
 94}_[human_hela_cells_mrna_partial_36
 u07223mrna_1930-2410,beta2-chimaerin_mrna_complete_cds
 u18932_4216-4756,heparan_sulfate-n-deacetylase/n-sulfotransferase_mrna_clone_hsst3'_3'_utr

- u26032_2176-2596,translation_initiation_factor_eif-2alpha_mrna_3'_utr_
u32581_2488-2884,lambda/iota-protein_kinase_c-interacting_protein_mrna_complete_cds_
u52700_70-328,tenascin-x_(xb)_mrna_race_clone_n1_partial_cds/gb=u52700_/ntype=rna
u62438_1545-1875,nicotinic_acetylcholine_receptor_beta3_subunit_precursor_mrna_complete_cds
- 5** u67932mrna_1128-
1700,camp_phosphodiesterase_(pde7a2)_mrna_complete_cds/gb=u67932_/ntype=rna_
u68488_1013-1397,5-hydroxytryptamine7_receptor_isoform_d_mrna_complete_cds
u85267_7-
145,down_syndrome_critical_region(dscr1)_gene_alternative_exon_1_partial_cds/gb=u85267_/n
- 10** all_x16667_1634-1917,hox2g_mrna_from_the_hox2_locus
all_x74987_2208-2684,mrna_for_2'-5'_oligoadenylate_binding_protein
all_x76040_2954-3309,mrna_for_lon_protease-like_protein
x76498exon#3_63-369:in_reversesequence_2899-3043,gene_for_uterine_bombesin_receptor
all_x78520_3490-3935,hsapiens_rna_for_clcn3
- 15** all_x81636_2127-2329,clathrin_light_chain_a_gene_
all_x81637_5805-5938,clathrin_light_chain_b_gene_
all_x91992_1340-1929,mrna_for_alkb_protein_homolog_
x93017exon_1293-1797,ncx2_gene_(exon_2)/gb=x93017_/ntype=dna_/annot=exon_
all_x96753_7313-7896,mrna_for_melanoma-associated_chondroitin_sulfate_proteoglycan_(mcsp)
- 20** all_y00064_1931-2418,mrna_for_secretogranin_i_(chromogranin_b)_
y08991cds_3846-4038:in_reversesequence_4743-4845,mrna_for_adaptor_protein_p150_
z34897_1138-1654,mrna_for_h1_histamine_receptor
- Metagene 239
- 25** ab000409_2046-2538,mrna_for_mnk1_complete_cds_
af000430_1941-2427,dynamin-like_protein_mrna_complete_cds
af009426_7540-8044,clone_22_mrna_alternative_splice_variant_beta-
1_complete_cds/gb=af009426_/ntype
- 30** d14660_739-1249,mrna_for_kiaa0104_gene_complete_cds_
d14878_1001-1499,mrna_for_protein_d123_complete_cds_
d38251_642-1149,mrna_for_rpb5_(xap4)_complete_cds_
d50678_3909-4413,mrna_for_apolipoprotein_e_receptor_2_complete_cds
d87448_4763-5183,mrna_for_kiaa0259_gene_partial_cds_
- 35** hg1102-ht1102_at_hg1102-ht1102_ras-related_c3_botulinum_toxin_substrate
hg3400-ht3579_at_hg3400-ht3579_nestin
hg4120-ht4392_s_at_hg4120-ht4392_protein_kinase_pitslre_alpha_altsplice_1-feb
hg944-ht944_s_at_hg944-ht944_dopamine_receptor_d4
j03626mrna#1_1151-1653_umps_gene_extracted_fromump_synthase_mrna_complete_cds_

- 102547_1290-1752,(clone_pz50-19)_cleavage_stimulation_factor_50kda_subunit_complete_cds
 177864_2060-2618,stat-like_protein(fe65)_mrna_complete_cds_
 m29580mrna_1813-2326,zinc-finger_protein(zfp7)_mrna_complete_cds_
 m81181_2360-2731,sodium/potassium_atpase_beta-2_subunit(atpb2)_mrna_complete_cds_
5 s81221_2246-2546,_lanosterol_synthase[human,_fetal_liver,_mrna_partial,_2637_nt]
 u07349_2331-2805,b_lymphocyte_serine/threonine_protein_kinase_mrna_complete_cds_
 u36221_1562-1814,pancreatic_zymogen_granule_membrane_protein_gp-2_mrna_complete_cds_
 u36787_491-995,putative_holocytochrome_c-type_synthetase_mrna_complete_cds
 u38864_1766-2186,zinc-finger_protein_c2h2-150_mrna_complete_cds_
10 u40271_3598-3999,transmembrane_receptor_precursor(ptk7)_mrna_complete_cds
 u41804_882-1254,putative_t1/st2_receptor_binding_protein_precursor_mrna_complete_cds
 u51903_5202-5712,rasgap-related_protein(iqgap2)_mrna_complete_cds
 u52969_19-505,pep19(pcp4)_mrna_complete_cds
 u71207_1846-2224,eyes_absent_homolog(eab1)_mrna_complete_cds.
15 u79256_655-1033,clone_23719_mrna_sequence
 all_v00594_15-75,mrna_for_metallothionein_from_cadmium-
 treated_cells,mrna_for_metallothionein_from_c
 all_x04434_4484-4971,mrna_for_insulin-like_growth_factor_i_receptor
 x07438exon#2_11-
20 166,dna_for_cellular_retinol_binding_protein(crbp)_exonsand/gb=x07438/_ntype=dna/_a
 x58199mrna_2491-2573,mrna_for_beta_adducin_
 all_x72304_1456-1688,mrna_for_corticotrophin_releasing_factor_receptor_
 x87344mrna#26_769-945,dma,dmb_hla-
 z1_ipp2_lmp2_tap1_lmp7_tap2_dob_dqb2_and_ring8_9,andgene
25 all_z14093_1190-1743,mrna_for_branched_chain_decarboxylase_alpha_subunit_

 Metagene 452

 m38180mrna_1319-1623,3-beta-hydroxysteroid_dehydrogenase/delta-5-delta-4-isomerase(3-beta-
30 hsd)_gene

 Metagene 395

 hg881-ht881_at_hg881-ht881_mucin_6;_gastric
35 l00190mrna_912-1384,antithrombin_iii(ataiii)_gene_exonand_complete_cds
 m16973mrna_1406-1910,complement_protein_c8_beta_subunit_mrna_complete_cds_
 all_m21642_180-
 301,(dysfunctional)_antithrombin_iii(atiii)_utah_gene,(dysfunctional)_antithrombin_i
 m26682_721-1171,t-cell_translocation_gene(ttg-1)_mrna_complete_cds_

- m54992_924-1494,b_cell_differentiation_antigen_mrna,_complete_cds
 m81883mrna_3226-3538,glutamate_decarboxylase_(gad67)_mrna,_complete_cds
 m83712_1078-1646,nicotinic_receptor_alphasubunit_mrna,_complete_cds.
 s75174_1316-1511,e2f-4=transcription_factor_[human,nalm6_and_hela_cells,_mrna,_1539_nt]
5 u16129_2108-2684,glutamate_receptor_(glur4)_mrna,_complete_cds.
 u50360_81-385,calcium,_calmodulin-
 dependent_protein_kinase_ii_gamma_mrna,_partial_cds/gb=u50360_/nty
 u79248_1157-1553,clone_23826_mrna_sequence_
 x51698cds_39-343:in_reversesequence,_387-465,spasmolytic_polypeptide_(sp)_mrna
10 all_x72925_3671-4008,mrna_for_desmocollin_type_1_
 x90828exon#2_233-752,mrna_for_transcription_factor,_lhx1_
 y11180mrna_31-247,mrna_for_twist_protein,_partial/gb=y11180_/ntype=rna_

 Metagene 84
15
 d28589mrna_281-743,mrna_(kiaa00167),_partial_sequence/gb=d28589_/ntype=rna_
 d79991_5181-5613,mrna_for_kiaa0169_gene,_partial_cds_
 l11573_1101-1665,surfactant_protein_b_mrna,_complete_cds/gb=l11573_/ntype=rna
 u79528_1038-1577,sr31747_binding_proteinmrna,_complete_cds

20
 Metagene 5

 m20030_68-612,small_proline_rich_protein_(sprii)_mrna,_clone_930_

25 Metagene 164

 af009674_2870-3308,axin_(axin)_mrna,_partial_cds
 d13748_812-1352,mrna_for_eukaryotic_initiation_factor_4ai
 d16562_514-1042,mrna_for_atp_synthase_gamma-subunit_(l-type),_complete_cds_
30 d28473_3882-4418,t-lymphocyte_mrna_for_ileucyl-trna_synthetase,_complete_cds_
 d29643_1079-1469,mrna_for_kiaa0115_gene,_complete_cds
 d32050_2761-3307,mrna_for_alanyl-trna_synthetase,_complete_cds_
 d42073_1551-2049,mrna_for_reticulocalbin,_complete_cds_
 d50063_1139-1553,mrna_for_proteasome_subunit_p40_/mov34_protein,_complete_cds_
35 d63478_2816-3308,mrna_for_kiaa0144_gene,_complete_cds
 d80000_5250-5754,mrna_for_kiaa0178_gene,_partial_cds_
 d86970_5998-6400,mrna_for_kiaa0216_gene,_complete_cds
 d87071_5779-6223,mrna_for_kiaa0233_gene,_complete_cds
 d87437_4613-5039,mrna_for_kiaa0250_gene,_complete_cds

- d89052_428-938,mrna_for_proton-atpase-like_protein,_complete_cds_
hg1153-ht1153_at_hg1153-ht1153_nucleoside_diphosphate_kinase_nm23-h2s
hg2279-ht2375_at_hg2279-ht2375_triosephosphate_isomerase_
j03191mrna_192-684,profilin_mrna,_complete_cds_
5 j04031_2529-3057,methylenetetrahydrofolate_dehydrogenase-
_methenyltetrahydrofolate_cyclohydrolase-fo
j04988cds_1925-2147:in_reversesequence,_7591-
7831,90_kd_heat_shock_protein_gene,_complete_cds_
110678_1128-1650,profilin_ii_mrna,_complete_cds
10 111669_1355-1715,tetracycline_transporter-like_protein_mrna,_complete_cds
114076_1469-2051,pre-mrna_splicing_factor_srp75_mrna,_complete_cds_
116842_1402-1792,ubiquinol_cytochrome-c_reductase_core_i_protein_mrna,_complete_cds
120010_7717-8185,hcf1_gene_related_mrna_sequence_
133243mrna_13655-14051,polycystic_kidney_diseaseprotein_(pkd1)_mrna,_complete_cds
15 138696_961-1375,autoantigen_p542_mrna,_3'_end_of_cds
m11433_115-403,cellular_retinol-binding_protein_mrna,_complete_cds_
m31606mrna_1102-1528,phosphorylase_kinase_(psk-c3)_mrna,_complete_cds
all_m34677_1486-1913,nested_gene_protein_gene,_complete_cds
m57567_491-953,adp-ribosylation_factor_(harf5)_mrna,_complete_cds
20 m61832_1472-2002,s-adenosylhomocysteine_hydrolase_(ahcy)_mrna,_complete_cds
m81601_2039-2483,transcription_elongation_factor_(sii)_mrna,_complete_cds
m86400_2239-2743,phospholipase_a2_mrna,_complete_cds_
m88458_585-1095,elp-1_mrna_sequence
m94362_3717-4179,lamin_b2_(lamb2)_mrna,_partial_cds
25 m97856_2016-2430,histone-binding_protein_mrna,_complete_cds_
s75463_1145-
1565_p43=mitochondrial_elongation_factor_homolog_[human,_liver,_mrna,_1644_nt]
all_u02493_2130-2485,54_kda_protein_mrna,_complete_cds_
u02619_6437-6965,tfiic_box_b-binding_subunit_mrna,_complete_cds_
30 u18321_1065-1569,ionizing_radiation_resistance_conferring_protein_mrna,_complete_cds_
u20285_1283-1811,gps1_(gps1)_mrna,_complete_cds
u25988_680-720,pregnancy-specific_glycoprotein(psg13')_mrna,_complete_cds_
u28386_1405-1933,nuclear_localization_sequence_receptor_hsrp1alpha_mrna,_complete_cds
u31556_1445-1679,transcription_factor_e2f-5_mrna,_complete_cds_
35 u33053_2381-2879,lipid-activated_protein_kinase_prk1_mrna,_complete_cds
u36764_721-997,tgf-beta_receptor_interacting_proteinmrna,_complete_cds
u39400_1407-1887,nof1_mrna,_complete_cds_
u47077_13025-13463,dna-dependent_protein_kinase_catalytic_subunit_(dna-
pkcs)_mrna,_complete_cds

- u51586_1262-1676,siah_binding_protein(siahbp1)_mrna,_partial_cds
u62136_660-1050,putative_enterocyte_differentiation_promoting_factor_mrna,_partial_cds_
u66711mrna_556-1102,ly-6-related_protein_-9804_gene,_complete_cds_
u73379_193-661,cyclin-selective_ubiquitin_carrier_protein_mrna,_complete_cds_
5 u81375_1669-2119,placental_equilibrative_nucleoside_transporter(hent1)_mrna,_complete_cds_
v00599mma_903-1380,mrna_fragment_encoding_beta-tubulin(from_clone_d-beta-1)_
all_x02152_1090-1625,mrna_for_lactate_dehydrogenase-a(ldh-a,_ec_1.1.1.27)_
all_x04366_2448-
2986,mrna_for_calcium_activated_neutral_protease_large_subunit_(mucanp,_calpain,_ec_
10 all_x05130_1362-1876,mrna_for_prolyl_4-hydroxylase_beta_subunit_(ec_1.14.11.2)_ (procollagen-1-
proline
all_x14850_1122-1555,h2a.x_mrna_encoding_histone_h2a.x_
all_x52142_2163-2734,mrna_for_ctp_synthetase_(ec_6.3.4.2)
x58079mma_43-565,mrna_for_s100_alpha_protein
15 x67951cds_312-576:in_reversesequence,_642-888,mrna_for_proliferation-associated_gene_(pag)_
all_x75208_3276-3781,hek2_mrna_for_protein_tyrosine_kinase_receptor
all_x97335_3247-3704,mrna_for_kinase_a_anchor_protein
y10807_650-1227,mrna_for_arginine_methyltransferase,_splice_variant,_1262_bp_
z27113cds_73-325:in_reversesequence,_439-463,gene_for_rna_polymerase_ii_subunit_14.4_kd_
20 z48501cds_957-1429,mrna_for_polyadenylate_binding_protein_ii/gb=z48501_/ntype=rna
z48950exon#4_794-1100,hh3.3b_gene_for_histone_h3.3_

Metagene 136

25 ac000064cds#2_102-372:in_fullsequence,_6375-
6621,_wugsc:h_rg083m05.2_gene_extracted_frombac_clone_rg
ac000064cds#1_1287-1581:in_reversesequence,_16950-
17160,_wugsc:h_rg083m05.2_gene_extracted_frombac_c
af000177_293-851,sm-like_protein_casm_(casm)_mrna,_complete_cds/gb=af000177_/ntype=rna
30 af000231_1768-2308,rab11a_gtpase_mrna,_complete_cds.
af015950_3501-3909,telomerase_reverse_transcriptase_(htrt)_mrna,_complete_cds.
d10656_988-1528,mrna_for_crk-ii,_complete_cds
d63391_341-773,mrna_for_platelet_activating_factor_acetylhydrolase_ib_gamma-
subunit,_complete_cds
35 d86959_5435-5867,mrna_for_kiaa0204_gene,_complete_cds
hg3104-ht3280_at_hg3104-ht3280_serine_protease_met1
l34820_566-938,nad+-dependent_succinate-semialdehyde_dehydrogenase_(ssadh)_mrna,_3'_end
m37400mrna_1352-1886,cytosolic_aspartate_aminotransferase_mrna,_complete_cds_
m63483_757-1255,major_nuclear_matrix_protein_mrna

- m68891_2398-2686,gata-binding_protein_(gata2)_mrna,_complete_cds_
s72370_3422-3962,_pyruvate_carboxylase_[human,_kidney,_mrna,_4017_nt]_
u01160_1056-1635,transmembranesuperfamily_protein_(sas)_mrna,_complete_cds_
u39412_675-1209:not_in_gb_record,platelet_alpha_snap_mrna,_complete_cds_
5 u44755_965-1487,pse-binding_factor_ptf_delta_subunit_mrna,_complete_cds_
u44839_2566-3088,putative_ubiquitin_c-terminal_hydrolase_(uhx1)_mrna,_complete_cds_
u66469_819-1209,cell_growth_regulator_cgr19_mrna,_complete_cds_
u87972_91-373,nad+-isocitrate_dehydrogenase_mrna,_partial_cds/gb=u87972_/ntype=rna_
all_x12433_1247-1734,phs1-2_mrna_with_orf_homologous_to_membrane_receptor_proteins_
10 all_x17025_1254-1807,homolog_of_yeast_ipp_isomerase

Metagene 262

- d90070_1329-1828,atl-derived_pma-responsive_(apr)_peptide_mrna_
15 m69181_6995-7523,nonmuscle_myosin_heavy_chain-b_(myh10)_mrna,_partial_cds_
u02680_2435-2837,protein_tyrosine_kinase_mrna,_complete_cds

Metagene 391

- 20** 176627mrna_5831-
6329,metabotropic_glutamate_receptoralpha_(mglur1alpha)_mrna,_complete_cds_
m55422_2463-2733,krueppel-related_zinc_finger_protein_(h-plk)_mrna,_complete_cds_
all_m61855_1535-1714,cytochrome_p4502c9_(cyp2c9)_mrna,_clone_25
all_x14968_1221-1636,testis_mrna_for_the_rii-alpha_subunit_of_camp_dependent_protein_kinase
25 x61079mrna_10-211,mrna_for_t_cell_receptor,_clone_igra24.
z16411cds_2917-3110:in_reversesequence,_3137-3441,mrna_encoding_phospholipase_c

Metagene 276

- 30** hg1067-ht1067_r_at_hg1067-ht1067_mucin_
u43292_706-1252,mds1b_(mds1)_mrna,_complete_cds_
all_x83492_418-500,mrna_for_fas/apo-1_(clone_pcrtm11-
fasdelta(4,7))/gb=x83492_/ntype=rna,mrna_for_fa
x95826cds_203-773,art4_gene/gb=x95826_/ntype=dna_/annot=cds
35 x99894_936-1482,mrna_coding_for_insulin_promoter_factor_1

Metagene 76

d50310_731-1127,mrna_for_cyclin_i,_complete_cds

- d87735_127-643,mrna_for_ribosomal_protein_114,_complete_cds
 hg1515-ht1515_f_at_hg1515-ht1515_transcription_factor_bt3b
 hg3117-ht3293_at_hg3117-ht3293_mps1
 hg384-ht384_at_hg384-ht384_ribosomal_protein_126_
- 5 hg429-ht429_at_hg429-ht429_b-cell_growth_factor_
 hg613-ht613_at_hg613-ht613_ribosomal_protein_s12_
 hg688-ht688_f_at_hg688-ht688_major_histocompatibility_complex_ii_dr_beta_2_
 j03459mrna_1459-1855,leukotriene_a-4_hydrolase_mrna,_complete_cds
 i08666_953-1421,porin (por) mrna,_complete_cds_and_truncated_cds
- 10 i36870mrna_3077-3533,map_kinase_kinase(mkk4)_mrna,_complete_cds
 m13934cds#2_41-407:in_reversesequence,_5551-
 5557,_rps14_gene (unknown protein)_extracted_fromribosom
 m14199_2-381,laminin_receptor_(2h5_epitope)_mrna,_5'_end_
 m17885mrna_532-946,acidic_ribosomal_phosphoprotein_p0_mrna,_complete_cds_
- 15 m26730cds_3-273:in_reversesequence,_99-204,mitochondrial_ubiquinone-
 binding_protein_gene,_5'_flank_w
 m75126_3159-3537,hexokinase(hk1)_mrna,_complete_cds_
 m84711_345-831,v-fos_transformation_effector_protein_(fte-1),_mrna_complete_cds
 u12404_111-651,csa-19_mrna,_complete_cds_
- 20 u14970_122-656,ribosomal_protein_s5_mrna,_complete_cds_
 u14972_103-499,ribosomal_protein_s10_mrna,_complete_cds
 u21049cds_61-319:in_reversesequence,_592-760,dd96_mrna,_complete_cds
 u58682_31-313,ribosomal_protein_s28_mrna,_complete_cds_
 u65092_324-774,melanocyte-specific_gene(msg1)_mrna,_complete_cds
- 25 u70323_3897-4401,ataxin-2_(sca2)_mrna,_complete_cds
 u70439_956-1407,silver-stainable_protein_ssp29_mrna,_complete_cds
 v01516cds_713-1044:in_reversesequence,_1070-
 1293,messenger_fragment_encoding_cytoskeletal_keratin_(t
 all_x04347_618-917,liver_mrna_fragment_dna_binding_protein_upi_homologue_(c-terminus)
- 30 x12671mrna_1450-
 1726,_hnmp_a1_protein_gene_extracted_fromgene_for_heterogeneous_nuclear_ribonucleop
 x15940cds_66-348:in_reversesequence,_379-385,mrna_for_ribosomal_protein_131_
 x16560cds_1-163:in_reversesequence,_13-
 295,cox_viic_gene_for_subunit_viic_of_cytochrome_c_oxidase_(e
- 35 x53777cds_81-435,i23_mrna_for_putative_ribosomal_protein_
 x55733cds_1611-1773:in_reversesequence,_1840-2056,initiation_factor_4b_cdna
 x55954cds_19-385:in_reversesequence,_427-433,mrna_for_hl23_ribosomal_protein_homologue
 x62691cds_13-343,mrna_for_ribosomal_protein_(homologous_to_yeast_s24)_
 x73460cds_725-1133:in_reversesequence,_1211,mrna_for_ribosomal_protein_13_

- x76013cds_1933-2257:in_reversesequence,_2328-2394,qsrhs_mrna_for_glutaminyl-trna_synthetase_
x80822cds_13-331:in_reversesequence,_56-578,mrna_for_orf
x80909cds_297-591:in_reversesequence,_694-754,alpha_nac_mrna
all_y00339_913-1465,mrna_for_carbonic_anhydrase_ii_(ec_4.2.1.1)
5 y08915_749-1235,mrna_for_alphaprotein_

Metagene 130

ab002315_4819-5347,mrna_for_kiaa0317_gene,_complete_cds/gb=ab002315/_ntype=rna_
10 ab002382_4858-5320,mrna_for_kiaa0384_gene,_complete_cds/gb=ab002382/_ntype=rna_
ac002115mrna#2_3349-
7559:not_in_gb_record,_cox6b_gene_(coxg)_extracted_fromdna_from_overlapping_chro
af002020_4090-4600,niemann-
pick_c_disease_protein_(npc1)_mrna,_complete_cds/gb=af002020/_ntype=rna
15 d14657_355-775,mrna_for_kiaa0101_gene,_complete_cds
d25248_4510-5050,randomly_sequenced_mrna_
d25304_4431-4701,mrna_for_kiaa0006_gene,_partial_cds_
d25547_779-864,mrna_for_pimt_isozyme_i,_complete_cds_
d28476_5899-6385,mrna_for_kiaa0045_gene,_complete_cds
20 d55716_1952-2378,mrna_for_plcdc47,_complete_cds
d63876_3171-3717,mrna_for_kiaa0154_gene,_partial_cds_
d79998_3100-3562,mrna_for_kiaa0176_gene,_partial_cds_
d83004_644-1148,epidermoid_carcinoma_mrna_for_ubiquitin-
conjugating_enzyme_e2_similar_to_drosophila_
25 d83785_5214-5634,mrna_for_kiaa0200_gene,_complete_cds
d85181_1502-2018,mrna_for_fungal_sterol-c5-desaturase_homolog,_complete_cds
d86550_5888-6338,mrna_for_serine/threonine_protein_kinase,_complete_cds
d87451_2622-3162,mrna_for_kiaa0262_gene,_complete_cds
d87969_1206-1686,mrna_for_cmp-sialic_acid_transporter,_complete_cds
30 hg2492-ht2588_at_hg2492-ht2588_glutamate_receptor_subunit
hg4557-ht4962_at_hg4557-ht4962_small_nuclear_ribonucleoprotein_u1,_lsnrp_
l07758_1288-1762,ief_ssp_9502_mrna,_complete_cds_
l13738mrna_4076-4490,activated_p21cdc42hs_kinase_(ack)_mrna,_complete_cds
all_l19314_3362-3789,hry_gene,_complete_cds
35 l20859_2655-3159,leukemia_virus_receptor(givr1)_mrna,_complete_cds
l21936_1796-2222,succinate_dehydrogenase_flavoprotein_subunit_(sdh)_mrna,_complete_cds_
l27706_1445-1985,chaperonin_protein_(tcp20)_gene_complete_cds
l34600_1958-2426,nuclear-encoded_mitochondrial_initiation_factormrna,_complete_cds
all_m22877_1917-2434,somatic_cytochrome_c_(hcs)_gene,_complete_cds_

- m29960mrna_1721-2141,steroid_receptor_(tr2-11)_mrna,_complete_cds
 m31932mrna_1771-2341,igg_low_affinity_fc_fragment_receptor_(fcγria)_mrna,_complete_cds_
 m32011mrna_1623-2157,neutrophil_oxidase_factor_(p67-phox)_mrna,_complete_cds_
 m33336_2441-3005,camp-dependent_protein_kinase_type_i-
 5 alpha_subunit_(prkar1a)_mrna,_complete_cds_
 m75715_1635-2185,tb3-1_mrna,_complete_cds
 u07559_1832-2366,isl-1_(islet-1)_mrna,_complete_cds
 u11872_36-72,interleukin-
 8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb1,_partial_cds/gb=u1187
 10 u15642_975-1472,transcription_factor_ε2f-5_mrna,_complete_cds
 u47927_2598-3132,isopectidase_t_(isot)_mrna,_complete_cds
 u48296_1629-2175,protein_tyrosine_phosphatase_ptpcaax1_(hptpcaax1)_mrna,_complete_cds
 u52154_2352-2610,g_protein-
 coupled_inwardly_rectifying_potassium_channel_kir3.4_mrna,_complete_cds_
 15 u63541mrna_431-977,mrna_expressed_in_hc/hcc_livers_and_molt-
 4_proliferating_cells,_partial_sequence
 u77456_2006-2414,nucleosome_assembly_proteinmrna,_complete_cds
 u84720_1431-1611,mrna_export_protein_rael_(rael)_mrna,_complete_cds
 u89336exon#34-35_35-
 20 87:not_in_gb_record,_unknown_gene_extracted_fromhla_iii_region_containing_notch4
 u94832_2732-2958,kh_type_splicing_regulatory_protein_ksrp_mrna,_complete_cds.
 u94836_3450-3894,erprot_213-21_mrna,_complete_cds
 all_x06272_2379-2854,mrna_for_docking_protein_(signal_recognition_particle_receptor)_
 all_x17567_432-1018,rna_for_snmp_protein_b
 25 all_x63741_3695-4230,pilot_mrna
 x66113cds_2199-2633:in_reversesequence,_2682-2729,mrna_for_pm/scl_100kd_nucleolar_protein_
 all_x67155_2735-3228,mrna_for_mitotic_kinesin-like_protein-1_
 all_x79888_965-1500,auh_mrna_
 x87613cds_1996-2236:in_reversesequence,_2780-
 30 2912,mrna_for_skeletal_muscle_abundant_protein_
 all_x95632_1680-1784,mrna_for_arg_protein_tyrosine_kinase-binding_protein
 y07707_1136-1634,mrna_for_itba4_gene/gb=y07707_/ntype=rna
 z84721cds#1_81-390:in_reversesequence,_15248-
 15488,dna_sequence_from_cosmid_gg1_from_a_contig_from_t
 35 reverse_z86000_20444-20634,dna_sequence_from_pac_151b14_on_chromosome_22q12-
 qter_contains_somatostat

Metagene 42

ab000462_6801-7227,mrna_for_sh3_binding_protein,_clone_res4-23a,_complete_cds
 m65062_1233-1527,insulin-like_growth_factor_binding_protein(igfbp-5)_mrna,_complete_cds_
 m93221mrna_4618-5110,macrophage_mannose_receptor_(mrc1)_gene_
 u25801_225-675,tax1_binding_protein_mrna,_partial_cds
5 all_x16699_2053-2130,mrna_for_cytochrome_p-450hp_
 x72177mrna_2964-3510,c6_gene,_exon_1

Metagene 427

10 m60459_1277-1745,erythropoietin_receptor_mrna,_complete_cds
 u45880_1969-2515,x-linked_inhibitor_of_apoptosis_protein_xiap_mrna,_complete_cds
 u89326_1533-1965,bone_morphogenetic_protein_receptor_type_i_alk-6_mrna,_complete_cds_
 all_x66610_1372-1697,mrna_for_enolase
 all_x78678_1384-1871,khk_mrna_for_ketohexokinase,_clone_phkhk3a

15

Metagene 230

all_d29675_1092-
 1149,inducible_nitric_oxide_synthase_gene,_promoter_and_exon/gb=d29675_/ntype=dna_/a
20 d29675exon_2-
 136,inducible_nitric_oxide_synthase_gene,_promoter_and_exon/gb=d29675_/ntype=dna_/annot
 hg2730-ht2827_s_at_hg2730-ht2827_fibrinogen,_a_alpha_polypeptide,_altsplice_2,_e_
 117128_1940-2480,(clone_h4/h16)_gamma-glutamic_carboxylase_mrna,_complete_cds_
 all_m10943_444-1929,metallothionein-if_gene_(hmt-if)_
25 m18731_at_m18731_m18731,not_in_gb_record,galactose-1-
 phosphate_uridylyltransferase_(galt)_mrna,_comple
 m81933_1920-2394,cdc25a_mrna,_complete_cds_
 s79862_1641-
 2226,_26_s_protease_subunit_5b=50_kda_subunit_[human,_hela_cells,_mrna_partial,_2253_nt]

30

u20734cds_709-1014:in_reversesequence,_7020-
 7258,transcription_factor_junb_(junb)_gene,_5'_region_an
 u43328_1158-1698,link_protein_mrna,_complete_cds_
 u52155_1646-2168,atp-

dependent_inwardly_rectifying_potassium_channel_kir4.1_mrna,_complete_cds_

35

u77664_417-891,masep_protein_p38_(rpp38)_mrna,_complete_cds.
 all_x79483_1063-1556,erk6_mrna_for_extracellular_signal_regulated_kinase_
 y07829exon#2_13-
 364,_exon_fromgene_encoding_ring_finger_protein/gb=y07829_/ntype=dna_/annot=exon,_ex
 all_y08765_1854-2207,mrna_for_splicing_factor,_sfl-h11_isoform_

Metagene 201

- reverse_ac000063_31010-31140,cosmid_clone_luca19_from_3p21.3_
- 5** hg1761-ht1778_s_at_hg1761-ht1778_tyrosine_kinase_fer_
hg2149-ht2219_at_hg2149-ht2219_mucin_
110338_953-1360,sodium_channel_beta-1_subunit_(scn1b)_mrna,_complete_cds_
120860_2219-2684,glycoprotein_ib_beta_mrna,_complete_cds_
m11186exon#3_20-134:not_in_gb_record,prepro-oxytocin-
- 10** neurophysin_i_(oxt)_gene,_complete_cds_
m29273_1749-2307,myelin-associated_glycoprotein_(mag)_mrna,_complete_cds_
m55040mrna_1689-2187,acetylcholinesterase_(ache)_mrna,_complete_cds
m64082_1605-2055,flavin-containing_monooxygenase_(fmo1)_mrna,_complete_cds_
m73481mrna_1227-1641,gastrin_releasing_peptide_receptor_(grpr)_mrna,_complete_cds
- 15** m76446_1521-1977,alpha-a1-adrenergic_receptor_mrna,_complete_cds_
m86546_1284-1716,pbx1a_and_pbx1b_mrna,_complete_cds
m88282mrna_4784-5180,tactile_protein_mrna,_complete_cds
s75578_755-1286,_4-
aminobutyrate_aminotransferase_[human,_neuroblastoma_be_cells,_mrna_partial,_1352
- 20** u18991_2113-2638,retinal_pigment_epithelium-
specific_61_kda_protein_(rpe65)_mrna,_complete_cds_
u37251_1908-2328,krab_zinc_finger_protein_(znf177)_mrna,_splicing_variant,_complete_cds
u38268cds_61-379,cytochrome_b_pseudogene,_partial_cds/gb=u38268/_ntype=dna/_annot=cds
u40990_2251-2797,voltage_gated_potassium_channel_(kvlqt1)_mrna,_complete_cds
- 25** u70663_1532-1928,zinc_finger_transcription_factor_hezf_(ezf)_mrna,_complete_cds
u78190mrna_159-687,gtp_cyclohydrolase_i_feedback_regulatory_protein_gene,_complete_cds
all_x00237_613-824,f_variable_segment_5'_to_antithrombin_iii_gene_(at_iii)_
x07495cds_389-764:in_reversesequence,_1383-1449,mrna_for_cp19_homeobox_from_hox-3_locus.
all_x51408_1626-2017,mrna_for_n-chimaerin
- 30** all_x75308_2091-2608,mrna_for_collagenase_3
x80062cds_1187-1268:in_reversesequence,_1430-1463,sa_mrna_

Metagene 190

- 35** 126584_3368-3933,(cdc25)_mrna,_complete_cds
s75168mrna_1515-2079,_matk=megakaryocyte-
associated_tyrosine_kinase_[human,_genomic,_2617_ntsegments
u02609_1934-2450,transducin-like_protein_mrna,_complete_cds
u07882_1382-1730,delta_opioid_receptor_mrna,_complete_cds

- u16307_996-1458,glioma_pathogenesis-related_protein_(glipr)_mrna,_complete_cds_
u59831mrna_1876-2385,transcription_factor,_forkhead_related_activator(freac-
4)_gene,_complete_cds
y10313_1352-1730:not_in_gb_record,mrna_for_nerve_growth_factor-inducible_pc4_homologue
5 all_z83741_654-1183,hh2a/m_gene

Metagene 69

- d85759_2398-2701,fetuses,_20-26_weeks_brain_mrna_for_mnb_protein_kinase,_complete_cds
10 hg2479-ht2575_s_at_hg2479-ht2575_helix-loop-helix_protein_sef2-1d
176528exon_146-615,presenilin(ps1;s182)_gene
m29551_2520-3054,calcineurin_a2_mrna,_complete_cds_
m83941_2764-3124,receptor_tyrosine_kinase_(hek)_mrna,_complete_cds_
s77154_1862-2362,_tinur=_ngfi-b/nur77_beta-
15 type_transcription_factor_homolog_[human,_t_lymphoid_cell
u17989_3352-3796,nuclear_autoantigen_gs2na_mrna,_complete_cds
u56244_at_u56244_u56244,not_in_gb_record,hig-1_mrna,_complete_cds_
u58091_427-883,hs-cul-4b_mrna,_partial_cds_
u69611_2905-2985,tnf-alpha_converting_enzyme_mrna,_complete_cds
20 u72648cds_1037-1354:in_reversesequence,_4177-4210,alpha2-c4-
adrenergic_receptor_gene,_complete_cds
u80456_3416-3788,transcription_factor_sim2_long_form_mrna,_complete_cds
u86755_2390-2735,tnf-alpha_converting_enzyme_mrna,_complete_cds
all_x79204_10002-10585,scal_mrna_for_ataxin
25 x83573_1377-1803,arse_mrna_
x84194cds_61-271:in_reversesequence,_501-
555,mrna_for_acylphosphatase,_erythrocyte_(ct)_isoenzyme_
x91196mrna#2_3588-4161,mrna_for_e14_and_a-t_proteins/gb=x91196/_ntype=rna
30 Metagene 178.
ab000895_25-385,mrna_for_cadherin_fib1,_partial_cds/gb=ab000895/_ntype=rna
all_d00408_1838-1946,fetal_liver_cytochrome_p-450_(p-
450_hfla),_complete_cds,fetal_liver_cytochrome_
35 d26018_2865-3381,mrna_for_kiaa0039_gene,_partial_cds_
d83646_1984-2452,mrna_for_metalloproteinase,_complete_cds
d83767_917-1319,clone_n9_rep-8_mrna,_complete_cds
d84307_1321-1813,cdna_for_phosphoethanolamine_cytidyltransferase,_complete_cds_
hg2714-ht2810_at_hg2714-ht2810_tyrosine_kinase_

- hg3893-ht4163_at_hg3893-ht4163_phosphoglucomutase_1_altsplice_
 112701cds_103-283:in_reversesequence, 325-463,engrailed_protein_(en2)_gene, 5'_end_
 137882_1340-1814,frizzled_gene_product_mrna_complete_cds
 141919mrna_1877-2450,hic-1_gene_fragment_
- 5** 176937mrna_4642-
 5098,unnamed_protein_product_gene_extracted_fromwerner_syndrome_gene_complete_cds
 all_m32053_2900-3489,h19_ma_gene_complete_cds_(spliced_in_silico)
 all_m58569_4044-4260,fibrinogen_alpha-
 subunit_bipartite_transcript_complete_cds_of_extended_(alpha-
- 10** m64710cds_64-353:in_reversesequence, 1226-1353,c-type_natriuretic_peptide_gene_complete_cds
 m77829_737-1269,channel-like_integral_membrane_protein_(chip28)_mrna_complete_cds_
 m81830cds_716-1040:in_reversesequence, 1170-
 1326,somatostatin_receptor_isoform(ssr2)_gene_complete
 u03399_1649-2147,t-complex_protein_10a_(tcp10a)_mrna_complete_cds_
- 15** u11287_5386-5932,n-methyl-d-aspartate_receptor_subunit_nr3_(hnr3)_mrna_complete_cds_
 u12622_4-
 358,beaded_intermediate_filament_protein_cp115_mrna_partial_cds/gb=u12622/_ntype=rna_
 u22314_2753-3311,rest_protein_mrna_complete_cds_
 u48436_5739-6290,fragile_x_mental_retardation_protein_fmr2p_(fmr2)_mrna_complete_cds
- 20** u50315_2179-2551,enhancer_of_zeste_homolog(ezh1)_mrna_complete_cds_
 all_u58658_522-1093,unknown_protein_mrna_within_the_p53_intron_1_complete_cds_
 u62431_2093-
 2633,nicotinic_acetylcholine_receptor_alpha2_subunit_precursor_mrna_complete_cds_
 u87460_3537-4113,putative_endothelin_receptor_type_b-like_protein_mrna_complete_cds_
- 25** u89335exon#30_375-
 909_notch4_gene_(notch4)_extracted_fromhla_iii_region_containing_notch4_(notch4)_
 x62429cds_438-784:in_reversesequence, 877-994,mrna_for_transcription_factor_pit-1_
 all_x75315_849-1348,seb4b_mrna_
 x83703mrna_1284-1854,mrna_for_cytokine_inducible_nuclear_protein_
- 30** all_z35102_2543-3018,mrna_for_ndr_protein_kinase_
 z48512exon#4_87-303,xg_mrna_(clone_pep6)/gb=z48512/_ntype=rna
 all_z83742_507-757,hh2a/c_gene.
- Metagene 162
- 35** hg3242-ht4231_s_at_hg3242-ht4231_calcium_channel_voltage-
 gated_alpha_1e_subunit_altsplice_3_
 hg4258-ht4528_at_hg4258-ht4528_kinase_inhibitor_p27kip1_cyclin-dependent
 hg4411-ht4681_at_hg4411-ht4681_mucin_gastric

- hg4677-ht5102_s_at_hg4677-ht5102_oncogene_ret/ptc2_fusion_activated_
k01900mrna_655-1213,lymphocyte_interferon_alpha_type_201_mrna_complete_cds
132961_1584-1679,4-aminobutyrate_aminotransferase_(gabat)_mrna_complete_cds_
178267mrna_2573-3113,par-5_mrna_probable_5'_end
- 5** m10612cds_17-275:in_reversesequence,_2926-3822:not_in_gb_record,apolipoprotein_c-
ii_gene_complete_c
m13686_388-897,pulmonary_surfactant-associated_protein_mrna_complete_cds_clone_mpsap-6a
m16591mrna_1446-1933,hemopoietic_cell_protein-
tyrosine_kinase_(hck)_gene_complete_cds_clone_lambda
- 10** m81829cds_915-1137:in_reversesequence,_1260-
1476,somatostatin_receptor_isoformgene_complete_cds_
s38953cds_611-820:in_reversesequence,_4446-4527_xa_[human_genomic,_6873_nt]
s79281_25-
463_pancratic_ribonuclease_[human_mrna_recombinant_partial,_491_nt]/gb=s79281_/ntype=rn
- 15** u25826cds_795-1017:in_reversesequence,_4190-
4436,transcription_factor_(sc1)_gene_complete_cds_
u29725_2517-2937,bmk1_alpha_kinase_mrna_complete_cds
u31986_877-1381,carilage-specific_homeodomain_protein_cart-1_mrna_complete_cds_
u36798_4071-4551,platelet_cgi-pde_mrna_complete_cds
- 20** u48936_15-139,amiloride-
sensitive_epithelial_sodium_channel_gamma_subunit_mrna_5'_end_partial_cds/
u49248_4807-
5251,canalicular_multispecific_organic_anion_transporter_(cmoat)_gene_complete_cds_
u49837_684-1218,lim_protein_mlp_mrna_complete_cds_
- 25** u53174_1639-2059,cell_cycle_checkpoint_control_protein_mrna_complete_cds
u56814_495-957,dnase_i_homologous_protein_(dhp2)_mrna_complete_cds
u60062_1060-1550,fez1-t_mrna_alternatively_spliced_form_complete_cds_
u63090_1303-1813,gal_beta-1,3_galnac_alpha-2,3_sialyltransferase_(st3gal_ii)_mrna_complete_cds
u79295_817-1345,clone_23961_mrna_sequence
- 30** all_x65857_1542-2053,hgmp07e_gene_for_olfactory_receptor_
x70070cds_954-1194:in_reversesequence,_1608-1800,mrna_for_neurotensin_receptor_
x77307cds_1244-1382:in_reversesequence,_1491-1701,mrna_for_5-ht2b_serotonin_receptor
all_x87160_2768-3339,mrna_for_gamma_subunit_of_epithelial_amiloride-
sensitive_sodium_channel_
- 35** all_x95095_487-1058,mrna_for_pdgfralpha_protein/gb=x95095_/ntype=ma
z26653cds_8896-9286:in_reversesequence,_9383-9509,mrna_for_laminin_m_chain_(merosin)
all_z37976_6411-6916,mrna_for_latent_transforming_growth_factor-beta_binding_protein_(ltbp-2)
all_z38133_5578-5993,mrna_for_myosin_
all_z49825_1747-2253,mrna_for_hepatocyte_nuclear_factoralpha

z70276cds_2-294,mrna_for_fibroblast_growth_factor(partial).
 z83805_199-463,mrna_for_axonemal_dynein_heavy_chain_(partial_id_hdhc8)

Metagene 148

5

d13644_4013-4523,mrna_for_kiaa0019_gene,_complete_cds
 l35545mrna_689-1223,endothelial_cell_protein_c/apc_receptor_(epcr)_mrna,_complete_cds_
 m33882_2348-2762,p78_protein_mrna,_complete_cds
 m60750cds_3-348,histone_h2b.1_(h2b)_gene,_complete_cds/gb=m60750_/ntype=dna_/annot=cds_
 10 u78798_1699-2203,tnf_receptor_associated_factor(traf6)_mrna,_complete_cds.
 all_y08319_1743-2272,mrna_for_kinesin-2
 y12556_427-877,mrna_for_AMP-activated_protein_kinase_beta-1/gb=y12556_/ntype=rna_

Metagene 165

15

af000959_759-1269,transmembrane_protein_mrna,_complete_cds
 d28364_4-
 118,mrna_for_annexin_ii,_5'_utr_(sequence_from_the_5'_cap_to_the_start_codon)/gb=d28364_/nt
 hg2239-ht2324_at_hg2239-ht2324_potassium_channel_protein_
 20 hg3075-ht3236_s_at_hg3075-ht3236_focal_adhesion_kinase_
 m28214_255-723,gtp-binding_protein_(rab3b)_mrna,_complete_cds_
 m91368_2656-3189,na+/ca+_exchanger_(cnc)_mrna,_complete_cds
 u79734_4119-4683,huntingtin_interacting_protein_(hip1)_mrna,_complete_cds
 x71345mrna_222-798,mrna_for_trypsinogen_iv_b-form
 25 all_x83535_1791-2208,mrna_for_membrane-type_matrix_metalloproteinase_

Metagene 120

l21998_15275-15677,intestinal_mucin_(muc2)_mrna,_complete_cds
 30 l26234mrna_298-
 796,apolipoprotein_b_mrna_editing_enzyme,_catalytic_polypeptide(apobec1)_mrna,_comple
 m55905_1340-1820,mitochondrial_nad(p)+_dependent_malic_enzyme_mrna,_complete_cds_
 m96956_2590-2639,(clone_cr-3)_teratocarcinoma-
 derived_growth_factor(tdgf3)_mrna,_complete_cds_
 35 u00952_488-998,clone_a9a2brb7_(cac)n/(gtg)n_repeat-containing_mrna_
 u01062mrna_8334-8778,typeinositol_1,4,5-trisphosphate_receptor_(itpr3)_mrna,_complete_cds_
 u17418_1591-2071,parathyroid_hormone/parathyroid_hormone-
 related_peptide_receptor_mrna,_complete_cds
 u31099_13-469,dp_prostanoid_receptor_(ptgdr)_mrna,_partial_cds.

- u33838_2-188,nf-kappa-
 b_p65delta3_mrna_spliced_transcript_lacking_exonsand_7_partial_cds/gb=u33838
 u40622_999-1449,xrcc4_mrna_complete_cds_
 u40705_2127-2625,telomeric_repeat_binding_factor_(trf1)_mrna_complete_cds
- 5** u66561_2158-2614,kruppel-related_zinc_finger_protein_(znf184)_mrna_partial_cds
 u90313_212-758,glutathione-s-transferase_homolog_mrna_complete_cds
 u94333_2877-3429,clq/mb1/spa_receptor_clqr(p)_mrna_complete_cds.
 x89576_1772-2255,mrna_for_putative_mt4-mmp_protein_
 z19002cds_1508-1994:in_reversesequence,_2075-2081,of_plzf_gene_encoding_kruppel-
10 like_zinc_finger_pro
- Metagene 32
- d85376exon_2003-2453,dna_for_thyrotropin-releasing_hormon_receptor_
15 hg1034-ht1034_f_at_hg1034-ht1034_atpase_na+/k+_transporting_alphapolypeptide
 hg1471-ht3923_s_at_hg1471-ht3923_transcription_factor_oct-1a/1b_altsplice_2_oct-1b_
 hg2147-ht2217_r_at_hg2147-ht2217_mucin_3_intestinal_
 hg3565-ht3768_at_hg3565-ht3768_zinc_finger_protein_
 all_k03431_5910-6163:not_in_gb_record_hpr_gene_(haptoglobin-
20 related_protein)_extracted_fromhaptoglo
 103840_2419-2970,fibroblast_growth_factor_receptor(fgfr4)_mrna_complete_cds
 107590_4754-5138,protein_phosphatase_2a_130_kda_regulatory_subunit_mrna_complete_cds
 111708_761-1205_humanbeta_hydroxysteroid_dehydrogenase_typemrna_complete_cds_
 113197_1853-2099,(clone_d21s418e)_pregnancy-associated_plasma_protein_a_(papp-
25 a)_gene,_5'_utr
 l27943mrna_291-867,cytidine_deaminase_(cda)_mrna_complete_cds
 l28821_4394-4838,alpha_mannosidase_ii_isozyme_mrna_complete_cds
 l40992mrna_906-1368,(clone_pebp2a1)_core-
 binding_factor_runt_domain_alpha_subunit(cbfa1)_mrna_3'
30 l49169mrna_3270-3612,g0s3_mrna_complete_cds_
 m14016mrna_644-947,uroporphyrinogen_decarboxylase_mrna_complete_cds_
 m14660exon_1123-1363:in_reversesequence,_1460-1646,isg-
 54k_gene_(interferon_stimulated_gene)_encodin
 m23892mrna_2101-2549,15-lipoxygenase_mrna_complete_cds
35 m27288exon_225-555:in_reversesequence,_567-768,oncostatin_m_gene
 m27783_2-433,neutrophil_elastase_mrna_3'_end
 m28213_94-627,gtp-binding_protein_(rab2)_mrna_complete_cds_
 m31525mrna_517-1081,mhc_ii_lymphocyte_antigen_(hla-dna)_gene_complete_cds_
 m55131mrna_5636-6134,cystic_fibrosis_transmembrane_conductance_regulator_(cftr)_gene_

- m55172_6712-7102,large_aggregating_cartilage_proteoglycan_core_protein_mrna_complete_cds
m63896cds_927-1197:in_reversesequence,_1866-
2022,transcriptional_enhancer_factor_(tefl)_dna_complet
m63967exon#2_1319-1625,mitochondrial_aldehyde_dehydrogenase_x_gene_complete_cds_
- 5** m80478exon#3_119-635,platelet_glycoprotein_ix_precursor_(gpix)_gene_complete_cds
m96995_497-1025,epidermal_growth_factor_receptor-binding_protein_grb2_(egfrbp-
grb2)_mrna_sequence_
s50017cds_904-1241:in_reversesequence,_444-505,_2'_3'_-cyclic_nucleotide_3'_-
phosphodiesterase_[hum
- 10** u07563_cds1_at_u07563_u07563,not_in_gb_record,abl_gene_exon_1b_and_intron_1b_and_putativ
e_m8604_me
u11861_511-949,g10_homolog_(edg-2)_mrna_complete_cds
u33841_8844-9294,ataxia_telangiectasia_(atm)_mrna_complete_cds
u34605_3365-3851,retinoic_acid_and_interferon-inducible_58k_protein_ri58_mrna_complete_cds_
- 15** u35246_1518-1962,vacuolar_protein_sorting_homolog_h-vps45_mrna_complete_cds_
u38980_841-972,pms2_related_(hpmsr6)_mrna_complete_cds
u43586_1531-2101,kinase_suppressor_of_ras-1_(ksr1)_mrna_partial_cds_
u43747_993-1425,frataxin_(frda)_mrna_complete_cds_
u50839_1969-2413:not_in_gb_record,g16_protein_(g16)_mrna_partial_cds.
- 20** u52513_1318-1642,rig-g_mrna_complete_cds
u65533_3076-3620,regulator_of_nonsense_transcript_stability_(rent1)_mrna_complete_cds_
u66828_2341-2500,carnitine_palmitoyltransferase_i_(cpti)_mrna_complete_cds
u70867_3444-3936,prostaglandin_transporter_hpgt_mrna_complete_cds_
u75362_2155-2557,isopeptidase_t-3_(isot-3)_mrna_complete_cds
- 25** u92971_1235-1805,protease-activated_receptor(par3)_mrna_complete_cds.
u93049_1841-2375,slp-76_associated_protein_mrna_complete_cds
x01038mrna_285-824,fetal_gene_for_apolipoprotein_ai_precursor_
x14445exon#3_240-702,int-2_proto-oncogene
all_x14789_1204-1793,alpha-a_crystallin_gene_exon_1,2_and_pseudoexon_
x15357cds_2853-3135:in_reversesequence,_3262-3454,mrna_for_natriuretic_peptide_receptor_(anp-
a_recep
x71874cds#1_268-739:in_reversesequence,_4531-4534,_proteasome-like_subunit_mec1-
l_gene_extracted_fro
x84746cds_544-1012,histo-blood_group_ab0_gene_exon_1
- 30** all_x85137_3131-3726,mrna_for_kinesin-related_protein
x98833mrna_3475-3937,mrna_for_zinc_finger_protein_hsall
all_y10260_1483-2048,eya1_gene_
z30643cds_1860-1921,mrna_for_chloride_channel_(putative)_2139bp
z46967cds_1216-1714,mrna_for_calicin_(partial)_
- 35**

Metagene 384

- 5 x92689cds_1457-1853,mrna_for_udp-galnac:polypeptide_n-acetylgalactosaminyl_transferase/gb=x92689_/nt

Metagene 392

- 10 d49728_2002-2330,nak1_mrna_for_dna_binding_protein,_complete_cds_
110717_6303-6332,t_cell-specific_tyrosine_kinase_mrna,_complete_cds_
125119_1561-2119,mu_opiate_receptor_(mor1)_mrna,_complete_cds
m32304_423-983,metalloproteinase_inhibitor_mrna,_complete_cds
m84526_470-890,adipsin/complement_factor_d_mrna,_complete_cds
u44103_339-559,small_gtp_binding_protein_rab9_mrna,_complete_cds.
15 u60319_2133-2643,hereditary_haemochromatosis_protein_hla-h_mrna,_complete_cds
u63825_269-737,hepatitis_delta_antigen_interacting_protein_a_(dipa)_mrna,_complete_cds_
u77735_1516-2026,pim-2_protooncogene_homolog_pim-2h_mrna,_complete_cds_
u90544_1665-2145,sodium_phosphate_transporter_(npt3)_mrna,_complete_cds
all_x76092_1925-2460,hrfx3_mrna
20 z22780cds_1528-1774:in_reversesequence,_1780-1870,cylicin_mrna_

Metagene 73

- ab000466_2465-2963,_clone_res4-24c,_exon_1,_2,_3
25 aj001487_25-265,mrna_for_transformation-sensitive_protein,_3'_utr/gb=aj001487_/ntype=rna
hg4755-ht5203_s_at_hg4755-ht5203_spinal_muscular_atrophy
j03260mrna_2076-2576,transducin_alpha-subunit_(gnaz)_mrna,_complete_cds
all_m20530_85-212,pancreatic_secretory_trypsin_inhibitor_(psti)_gene_
m59911_4048-4612,integrin_alpha-3_chain_mrna,_complete_cds_
30 m62400_1400-1928,gamma-aminobutyric_acid_receptor_type_a_rho-1_subunit_(gaba-a_rho-1)_mrna,_complete
m74826_1928-2396,glutamate_decarboxylase_(gad-2)_mrna,_complete_cds
all_u01317_19502-63478,_epsilon-globin_gene_extracted_frombeta_globin_region_on_chromosome_11,_epsil
35 u13220_1586-2066,forkhead_protein_freac-2_mrna,_partial_cds
u54999_1795-2287,lgn_protein_mrna,_complete_cds
all_x00734_8016-8239,beta-tubulin_gene_(5-beta)_with_ten_alu_family_members
x65293cds_1670-2180,mrna_for_protein_kinase_c-epsilon
all_x71348_2835-3436,vhnfl-c_mrna

all_x76057_1206-1765,pmil_mrna_for_phosphomannose_isomerase
 all_x98311_1901-2274,mrna_for_carcinoembryonic_antigen,_cgm2_
 z49205mrna_2454-2976,mrna_for_purinergic_receptor

5 Metagene 428

hg3344-ht3521_at_hg3344-ht3521_ubiquitin-conjugating_enzyme_ubch5
 all_m35999_3904-4463,platelet_glycoprotein_iiia_(gp11a)_mrna,_complete_cds
 all_u19906_5284-5711,arginine_vasopressin_receptor(avpr1)_gene,_complete_cds
 10 u54617_1233-1737,pyruvate_dehydrogenase_kinase_isoformmrna,_complete_cds
 x94703cds_244-628:in_reversesequence,_640-748,rab28_mrna

Metagene 224

15 hg3859-ht4129_at_hg3859-ht4129_mage-4a_antigen_
 u61741_25-137,clone(hl-
 18),_dynein_heavy_chain_(dnahc14)_mrna,_partial_cds/gb=u61741_/ntype=rna
 u67784_1106-1640,orphan_g_protein-coupled_receptor_(rdc1)_mrna,_partial_cds

20 Metagene 437

all_m73548_9853-10274,polyposis_locus_(dp2.5_gene)_mrna,_complete_cds
 u30245exon_3-
 56,myelomonocytic_specific_protein_(mnda)_gene,_5' flanking_sequence_and_complete_exon/
 25 u36448_1252-1792,ca2+-dependent_activator_protein_for_secretion_mrna,_complete_cds_
 u41737_103-
 523,pancreatic_beta_cell_growth_factor_(ingap)_mrna,_complete_cds/gb=u41737_/ntype=rna
 u48697_1787-2276,mariner-like_element-containing_mrna,_clone_pchmt2
 x89986cds_271-387:in_reversesequence,_794-1043,mrna_for_nbk_apoptotic_inducer_protein_

30

Metagene 216

l01087_2189-2693,protein_kinase_c-theta_(prkct)_mrna,_complete_cds_
 m16652mrna_324-
 35 858,pancreatic_elastase_ii_mrna,_complete_cds,pancreatic_elastase_ii_mrna,_complete
 m27691_1901-2417,transactivator_protein_(creb)_mrna,_complete_cds
 m94893_989-1499,testis-specific_protein_(tspy)_mrna,_3' end,_clone_pja923
 u30610_239-749,cd94_protein_mrna,_complete_cds_
 all_x17094_3675-4180,fur_mrna_for_furin

x55019cds_1128-1521:in_reversesequence,_1538-
1701,mrna_for_acetylcholine_receptor_delta_subunit.

Metagene 449

5

d79988_6383-6899,mrna_for_kiaa0166_gene,_complete_cds
d80001_4465-4939,mrna_for_kiaa0179_gene,_partial_cds_
d87450_5572-6034,mrna_for_kiaa0261_gene,_partial_cds_
hg2573-ht2669_at_hg2573-ht2669_zinc_finger_protein_kup_

10

m22638exon#4_154-682,lyl-1_protein_gene,_complete_cds
m62402_453-927,insulin-like_growth_factor_binding_protein(igfbp6)_mrna,_complete_cds
m85164_1354-1852,srf_accessory_protein_1b(sap-1)_mrna,_complete_cds
s79873_3394-3969,h-lamp-2=lysosome-associated_membrane_protein-
2_{alternatively_spliced}_[human,_li

15

u15174_224-746,nip3_(nip3)_mrna,_complete_cds
u24186cds_465-747:in_reversesequence,_1223-
1391,replication_protein_a_complex_subunit_homolog_rpa4_g
u34976_1059-1575,gamma-sarcoglycan_mrna,_complete_cds
u47677mrna_2495-2636,transcription_factor_e2f1(e2f1)_gene_promoter_and_

20

u59914_802-1240,chromosomemad_homolog_smad6_mrna,_complete_cds_
u80628_2216-2588,thymidine_kinaseisoform_b(tk2)_mrna,_alternatively_spliced,_partial_cds_
all_x16323_5339-5814,mrna_for_hepatocyte_growth_factor(hgf)_
x52009cds_813-1315:in_reversesequence,_1629,alpha-
1_strychnine_binding_subunit_of_inhibitory_glycine

25

Metagene 491

hg3510-ht3704_at_hg3510-ht3704_v-erba_related_ear-3_protein
hg880-ht880_s_at_hg880-ht880_mucin_6_gastric

30

u37519_2304-2784,aldehyde_dehydrogenase(aldh8)_mrna,_complete_cds_
all_x98263_520-1019,mrna_for_m-phase_phosphoprotein,_mpp6

Metagene 429

35

d13628_2506-2998,mrna_for_kiaa0003_gene,_complete_cds
hg2171-ht2241_r_at_hg2171-ht2241_12-lipoxygenase_
l47726_2090-2552,phenylalanine_hydroxylase(pah)_mutant_q20stop_mrna
all_m11591_5495-6174:in_m11591cds_567-598,mhc_ii_hla-sx-alpha_gene
u55764_784-1072,estrogen_sulfotransferase_mrna,_partial_cds

all_x51362_2101-2583,mrna_for_dopamine_d2_receptor_
x60708mrna_2812-3364,pchdp7_mrna_for_liver_dipeptidyl_peptidase_iv_

Metagene 210

5

j04111exon#1_2735-3251,c-jun_proto_oncogene_(jun),_complete_cds,_clone_hcj-1_
m19154mrna_2143-2503,transforming_growth_factor-beta-2_mrna,_complete_cds
m55210mrna#1_7322-7844,laminin_b2_chain_(lamb2)_gene_
m93426_7455-7845,protein_tyrosine_phosphatase_zeta-polypeptide_(ptprz)_mrna,_complete_cds
10 u04636mrna_3882-4386,cyclooxygenase-2_(hcox-2)_gene,_complete_cds_
u32114_756-1278,caveolin-2_mrna,_complete_cds
u60805_3576-4146,oncostatin-m_specific_receptor_beta_subunit_(osmrp)_mrna,_complete_cds

Metagene 208

15

d14686mrna_1554-2046,gene_for_glycine_cleavage_system_t-protein
d14695_1259-1817,mrna_for_kiaa0025_gene,_complete_cds
d23673_1204-

20

1666,_clone_hh109_(screened_by_the_monoclonal_antibody_of_insulin_receptor_substrate-1_(
d86965_6166-6490,mrna_for_kiaa0210_gene,_complete_cds
d89667_440-1004,mrna_for_c-myc_binding_protein,_complete_cds_
hg2379-ht3996_s_at_hg2379-ht3996_serine_hydroxymethyltransferase,_cytosolic,_altsplice_2_
hg270-ht270_at_hg270-ht270_lymphocyte_chemoattractant_factor_
hg2868-ht3012_s_at_hg2868-ht3012_xe7_pseudoautosomal_gene,_altsplice_2

25

hg371-ht1063_s_at_hg371-ht1063_mucin_1,_epithelial,_altsplice_6
hg3936-ht4206_at_hg3936-ht4206_interleukinreceptor
j00287exon#1_8-248:not_in_gb_record,pepsinogen_gene_
102867_2179-2689,62_kda_paraneoplastic_antigen_mrna,_3'_end_
113744_2775-3345,af-9_mrna,_complete_cds_

30

114927exon#7_1-159:in_reversesequence,_5382-
5676,tear_prealbumin_(tp)_gene,_complete_cds_and_promote
l38935mrna_564-1026,gt212_mrna
m14218mrna_1044-1440,argininosuccinate_lyase_mrna,_complete_cds
m38449_40-599,transforming_growth_factor-beta_mrna,_complete_cds,_clone_ptgf-beta-trp114_

35

m57763_731-1151,adp-ribosylation_factor_(harf6)_mrna,_complete_cds_
m60278_1771-2221,heparin-binding_egf-like_growth_factor_mrna,_complete_cds_
m79462_3853-4333,pml-1_mrna,_complete_cds
m91196_938-1513,dna-binding_protein_mrna,_complete_cds_
m96326mrna_370-886,azurocidin_gene,_complete_cds

- m96739_1964-2510,nscl-1_mrna_sequence
s72043mrna_5-68,_gif=growth_inhibitory_factor_[human_brain_genomic_2015_nt]_
s82362_1119-1690,_hrar-beta_2=retinoic-acid-
receptor_beta/suspected_tumor_suppressor_{5'_region,_tr
- 5** u03494_2213-2393,transcription_factor_lsf_mrna_complete_cds_
u05875_1655-2105,clone_psk1_interferon_gamma_receptor_accessory_factor-1_(af-
1)_mrna_complete_cds_
u40714_692-1142,tyrosyl-trna_synthetase_mrna_complete_cds/gb=u40714_/ntype=rna
u41068cds_2-268:in_reversesequence_944-
- 10** 1155,retinoid_x_receptor_beta_(rxrbeta)_gene_partial_3'_tra
u47101_428-758,nifu-like_protein_(hnifu)_mrna_partial_cds_
u52112mrna#1_3929-
4463,xq28_genomic_dna_in_the_region_of_the_11cam_locus_containing_the_genes_for_ne
u54644_1437-1806,tub_homolog_mrna_complete_cds
- 15** u58087_2096-2462,hs-cul-1_mrna_complete_cds_
u62531_3465-4029,ae2_anion_exchanger_(slc4a2)_mrna_complete_cds_
u65785_4028-4442,150_kda_oxygen-regulated_protein_orp150_mrna_complete_cds
u72515_1279-1811,c3f_mrna_complete_cds
u79255_760-1180,x11_protein_mrna_partial_cds
- 20** all_x13451_84-268,mrna_for_lymphocyte_lineage-restricted_mb-1_membrane_glycoprotein_c-
term(m-mb-1_ho
x13973cds_996-1356:in_reversesequence_1770-
1896,mrna_for_ribonuclease/angiogenin_inhibitor_(rai)_
all_x16135_1552-2003,mrna_for_novel_heterogeneous_nuclear_rnp_protein_1_protein_
- 25** x66362cds_743-1097:in_reversesequence_1121-1217,mrna_pctaire-
3_for_serine/threonine_protein_kinase_
all_x80818_3601-3860,mrna_for_metabotropic_glutamate_receptor_type_4_
x85106_2196-2712,mrna_for_ribosomal_s6_kinase
- 30** Metagene 160
- d14811_644-1124,mrna_for_kiaa0110_gene_complete_cds_
d14889_760-1240,mrna_for_small_gtp-binding_protein_s10_complete_cds
d21878_816-1386,mrna_for_bst-1_complete_cds_
- 35** hg3288-ht3465_at_hg3288-ht3465_xanthine_dehydrogenase
j04102_1830-2184,erythroblastosis_virus_oncogene_homolog(ets-2)_mrna_complete_cds
l25798_1061-1589,3-hydroxy-3-methylglutaryl_coenzyme_a_synthase_mrna_complete_cds
l41349mrna_3238-3646,phospholipase_c_beta(plcb4)_mrna_complete_cds
m17219_758-1286,brain_guanine_nucleotide-binding_protein_alpha-i_subunit_mrna_5'_end

u55054_3199-3697,k-cl_cotransporter_(hkcc1)_mrna,_complete_cds_
 u57094_502-1018,small_gtp-binding_protein_mrna,_complete_cds_
 u93091_4410-4806,toll_protein_homolog_mrna,_complete_cds_and_line-
 1_reverse_transcriptase_homolog,_p

5

Metagene 156

- hg2887-ht3031_r_at_hg2887-ht3031_sry-related_hmg-boxprotein
 hg4099-ht4369_s_at_hg4099-ht4369_adrenergic_receptor,_alpha_1b_
- 10 104947_3659-
 4199,(clones_bt3.081.8,_bt3.129.5_and_bt4.169)_receptor_tyrosine_kinase_(kdr)_mrna,_3'_e
 m74088_8374-8717,apc_gene_mrna,_complete_cds_
 m96738cds_719-1221,somatostatin_receptor_subtype(sstr3)_gene,_complete_cds
 m99435_2069-2325,transducin-like_enhancer_protein_(tle1)_mrna,_complete_cds
- 15 s72487_1134-1582,_orf1_5'_to_pd-ecgf/tp...orf2_5'_to_pd-
 ecgf/tp_[human,_epidermoid_carcinoma_cell_li
 u28043_1989-2499,plasma_membrane_na+/h+_exchanger_isoform(nhe3)_mrna,_complete_cds
 u28049_1684-2221,tbx2_(tbx2)_mrna,_complete_cds
 u51003_2591-3169,dlx-2_(dlx2)_mrna,_complete_cds_
- 20 u62739_986-1430,branched-chain_amino_acid_aminotransferase_(eca40)_mrna,_complete_cds
 u72509mrna_2-255,alternatively_spliced_b8_(b7)_mrna,_partial_sequence/gb=u72509_/ntype=ma_
 u79300_930-1404,clone_23629_mrna_sequence
 all_x69654_4-422,mrna_for_ribosomal_protein_s26
 x79439cds_16-277,notchdna_sequence/gb=x79439_/ntype=dna_/annot=cds
- 25 x82850cds_722-1090:in_reversesequence,_1108-1238,mrna_for_thyroid_transcript_factor_1_
 y00414cds_1266-1537:in_reversesequence,_1573-1785,mrna_for_tyrosine_hydroxylase_type_3
 all_y08265_1306-1834,mrna_for_dan26_protein,_partial_
 z49254cds_75-435:in_reversesequence,_549-651,l23-related_mrna_

30 Metagene 149

- d00097exon#2_152-710,serum_amyloid_p_component_(sap)_gene_with_upstream_promoter_
 d14533_812-1322,mrna_for_xpac_protein
 d16815_1642-2086,mrna_for_ear-1r,_complete_cds_
- 35 d87683_6419-6941,mrna_for_kiaa0243_gene,_partial_cds_
 hg2510-ht2606_at_hg2510-ht2606_ras-specific_guanine_nucleotide-releasing_factor
 j00314mrna#1_4079-4173,beta-tubulin_gene,_clone_m40
 j05200mrna_14740-15238,ryanodine_receptor_mrna,_complete_cds
 l11329_1162-1630,protein_tyrosine_phosphatase_(pac-1)_mrna,_complete_cds

- 112760exon#9_396-
 721,phosphoenolpyruvate_carboxykinase_(pck1)_gene,_complete_cds_with_repeats
 all_135263_3222-3721,csaids_binding_protein_(csbp1)_mrna,_complete_cds_
 m22976mrna_21-303:in_reversesequence,_668-728,cytochrome_b5_mrna,_3'_end
 5 m62397_3586-4126,colorectal_mutant_cancer_protein_mrna,_complete_cds_
 all_m83554_3167-3576,lymphocyte_activation_antigen_cd30_mrna,_complete_cds_
 m84424exon_1073-1217,cathepsin_e_(ctse)_gene_
 all_m93311_1950-2085,metallothionein-iii_gene,_complete_cds
 s83549_19-571,_na⁺/h⁺_exchanger_isoform_nhe-
 10 2_[human,_various_tissues,_mrna_partial,_595_nt]/gb=s835
 u02082_1643-2201,guanine_nucleotide_regulatory_protein_(tim1)_mrna,_complete_cds_
 u14528_2357-2807,sulfate_transporter_(dtd)_mrna,_complete_cds
 u18009_1900-2338,chromosome_17q21_mrna_clone_1f113_
 u19517_1692-2010,(apoargc)_long_mrna,_complete_cds_
 15 u22680_6048-6558,x2_box_repressor_mrna,_complete_cds_
 u36601_2620-3166,heparan_n-deacetylase/n-sulfotransferase-2_mrna,_complete_cds_
 u49436_1303-1783,translation_initiation_factor(eif5)_mrna,_complete_cds_
 u53003_1093-1609,gt335_mrna,_complete_cds
 u73338_6615-7113,methionine_synthase_mrna,_complete_cds
 20 u73682_2255-2651,meningioma-expressed_antigen(meal1)_mrna,_partial_cds_
 u78876_1789-2317,mek_kinase_mrna,_complete_cds_
 u80811_1092-1536,lysophosphatidic_acid_receptor_homolog_mrna,_complete_cds_
 x02176cds_1397-1656:in_reversesequence,_1681-
 1859,mrna_fragment_for_complement_component_c9
 25 x05997cds#1_726-1158:in_reversesequence,_1280-1316,mrna_for_gastric_lipase
 x51956mrna_1881-2397,eno2_gene_for_neuron_specific_(gamma)_enolase
 all_x60483_975-1171,h4/d_gene_for_h4_histone_
 x67325cds_31-337:in_reversesequence,_43-541,p27_mrna
 x67683cds_34-319:in_reversesequence,_13,mrna_for_keratin/gb=x67683/_ntype=rna
 30 x68149exon#2_2249-2687,blr1_gene_for_burkitt_lymphoma_receptor_1_
 x85133mrna_2399-2897,rbq-1_mrna
 x85372cds_18-210:in_reversesequence,_19-115,mrna_for_sm_protein_f_
 all_x87342_2921-3456,mrna_for_giant_larvae_homolog_
 x90908cds_11-353,mrna_for_i-15p_(i-babp)_protein_
 35 all_y00978_2012-2535,mrna_for_dihydrolipoamide_acetyltransferase_(pdc-e2)_(ec_2.3.1.12)
 y12393_346-819,mrna_for_srp1-like_protein,_partial_
 z24459exon#1_13-
 199,_exon2a_frommtcp1_gene,_exons_2a_to(and_joined_mrna)/gb=z24459/_ntype=dna/_annot

Metagene 125

- d14827_1564-1966,mrna_for_tax_helper_protein_1,_complete_cds_
all_d26561_2433-
- 5 3022,_orf_for_l1_protein_gene_extracted_frompapillomavirus_5b_genome_integrated_into
l34060_2124-2502,cadherin-8_mrna,_complete_cds
m94167_1894-2326,heregulin-beta2_gene,_complete_cds
s83390_2318-2865,_t3_receptor-associating_cofactor-1_[human,_fetal_liver,_mrna,_2930_nt]
u03398_1069-1576,receptor_4-1bb_ligand_mrna,_complete_cds
- 10 u52152_2642-3020,inwardly_rectifying_potassium_channel_kir3.3_mrna,_complete_cds_
u64871cds_870-1212:in_reversesequence,_1665-1773,putative_g_protein-
coupled_receptor_(gpr19)_gene,_c
u95626mrna#2_1641-
2133,_ccr2_gene_(ccr2a)_extracted_fromccr2b_(ccr2),_ccr2a_(ccr2),_ccr5_(ccr5)_and_
15 x77094cds_634-994:in_reversesequence,_1136-1214,mrna_for_p40phox

Metagene 71

- ab000220_4588-5134,mrna_for_semaphorin_e,_complete_cds_
20 109749_1019-1463,(clone_f4)_transmembrane_protein_mrna_sequence_
m87313_793-1335,myotonin_protein_kinase_(dm)_mrna_
u04520mrna_6221-6641,type_iv_collagen_a5_chain_(col4a5)_gene_
all_x87904_4159-4670,mrna_for_sep_protein
z78285_3-137,mrna_(clone_la7)

25

Metagene 374

- ab000896_49-391,mrna_for_cadherin_fib2,_partial_cds/gb=ab000896/_ntype=rna
ac002115mrna#1_932-
- 30 1448,_cox6b_gene_(coxg)_extracted_fromdna_from_overlapping_chromosomecosmids_r313
d29641_2800-3292,mrna_for_kiaa0052_gene,_partial_cds_
d83699_623-1001,brain_3'_utr_of_mrna_for_neuronal_death_protein,_partial_sequence
d86960_5652-6168,mrna_for_kiaa0205_gene,_complete_cds
hg2152-ht2222_at_hg2152-ht2222_zinc_finger_protein_92
- 35 hg3707-ht3922_f_at_hg3707-ht3922_guanine_nucleotide-
binding_protein,_alpha_inhibiting_activity_polyp
l13994_2830-3196,prec_gene,_complete_cds;_orf_x,_complete_cds_
l22343_1136-1517,nuclear_phosphoprotein_mrna,_complete_cds_
l41607mrna_1772-2330,beta-1,6-n-acetylglucosaminyltransferase_(ignt)_gene

- all_m11437_1562-2440;in_m11437cds#1_1198-
 1226, kng_gene_(kininogen)_extracted_fromkininogen_gene_kn
 m27533_883-1451,ig_rearranged_b7_protein_mrna_vc1-region,_complete_cds.
 m61764mrna_1015-1495,gamma-tubulin_mrna,_complete_cds
- 5** m65085_1792-2302,follicle_stimulating_hormone_receptor_mrna,_complete_cds
 m81778_2123-2689,serotonin_5-ht1c_receptor_mrna,_complete_cds
 s66541cds_375-687;in_reversesequence,_99-314,_b-
 50=neural_phosphoprotein_[human,_genomic,_1845_ntseg
 u03911_2485-3013,mutator_gene_(hms2)_mrna,_complete_cds_
- 10** u22816_3784-4288,lar-interacting_protein_1b_mrna,_complete_cds_
 u51095_1230-1656,homeobox_protein_cdx1_mrna,_complete_cds
 u59748_28-187,desert_hedgehog_(hdhh)_mrna,_partial_cds/gb=u59748_/ntype=rna
 u61538_199-751,calcium-binding_protein_chp_mrna,_complete_cds
 u74324_1797-2349,guanine_nucleotide_exchange_factor_mss4_mrna,_complete_cds
- 15** u81787_1686-2238,wnt10b_mrna,_complete_cds.
 u90437_43-259,rp1_homolog_mrna,_3'_utr_region/gb=u90437_/ntype=rna_
 all_x04391_1779-2320,mrna_for_lymphocyte_glycoprotein_t1/leu-1_
 x15673mrna_623-1121,ptr2_mrna_for_repetitive_sequence/gb=x15673_/ntype=rna_
 all_x15949_1543-2144,mrna_for_interferon_regulatory_factor-2_(irf-2)_
- 20** x56667mrna_915-1341,mrna_for_calretinin
 x78924cds_55-466;in_reversesequence,_622-631,hzfl_mrna_for_zinc_finger_protein
 x97630_2420-2897,mrna_for_serine/threonine_protein_kinase_emk
 all_x99657_783-1318,mrna_for_protein_containing_sh3_domain,_sh3gl2_
- 25** Metagene 168
- d00761_252-750,mrna_for_proteasome_subunit_hc5_
 d00762_237-777,mrna_for_proteasome_subunit_hc8_
 d13435_526-832,mrna_for_pig-f_(phosphatidyl-inositol-glycan_f),_complete_cds_
- 30** d13969_1638-2148,mrna_for_mel-18_protein,_complete_cds_
 d29677_5709-6231,mrna_for_kiaa0054_gene,_complete_cds
 d31762_6385-6775,mrna_for_kiaa0057_gene,_complete_cds
 d31766_2024-2552,mrna_for_kiaa0060_gene,_complete_cds
 d38449_2311-2791,mrna_for_g_protein-coupled_receptor,_complete_cds_
- 35** d38535_2583-2973,mrna_for_pk-120_
 d43950_1355-1739,mrna_for_kiaa0098_gene,_partial_cds_
 d50487_3756-4098,mrna_for_rna_helicase_(hrh1),_complete_cds
 d50863_1908-2370,mrna_for_tesk1,_complete_cds
 d50922_1972-2452,mrna_for_kiaa0132_gene,_complete_cds

- d50923_5018-5528,mrna_for_kiaa0133_gene,_complete_cds
d78586_6497-6923,cad_mrna_for_multifunctional_protein_cad,_complete_cds
d79993_2741-3167,mrna_for_kiaa0171_gene,_complete_cds
d79997_1881-2415,mrna_for_kiaa0175_gene,_complete_cds
5 d80010_4778-5198,mrna_for_kiaa0188_gene,_partial_cds_
d83776_4596-5166,mrna_for_kiaa0191_gene,_partial_cds_
d83782_3411-3915,mrna_for_kiaa0199_gene,_partial_cds_
d84557_2412-2874,mrna_for_hsmcm6,_complete_cds_
d86968_4437-4899,mrna_for_kiaa0213_gene,_partial_cds_
10 d86971_4851-5325,mrna_for_kiaa0217_gene,_partial_cds_
d86976_3592-4060,mrna_for_kiaa0223_gene,_partial_cds_
hg1019-ht1019_at_hg1019-ht1019_serine_kinase_psk-h1
hg1879-ht1919_at_hg1879-ht1919_ras-like_protein_tc10
hg2190-ht2260_at_hg2190-ht2260_crystallin_beta_b3_
15 hg2379-ht3997_s_at_hg2379-ht3997_serine_hydroxymethyltransferase,_cytosolic,_altsplice_3_
hg2649-ht2745_s_at_hg2649-ht2745_serine/threonine_protein_kinase_cdk3
hg3033-ht3194_r_at_hg3033-ht3194_spliceosomal_protein_sap_62_
hg3327-ht3504_s_at_hg3327-ht3504_dna-binding_protein_hrfx2_
hg3945-ht4215_at_hg3945-ht4215_phospholipid_transfer_protein_
20 hg4094-ht4364_s_at_hg4094-ht4364_transcription_factor_lsf-id_
hg4433-ht4703_at_hg4433-ht4703_cyclin_d1_promoter
hg511-ht511_at_hg511-ht511_ras_inhibitor_inf_
all_j03764_14604-15049_human_plasminogen_activator_inhibitor-1_gene_exonsto_9_
l04953_2585-3065,x11_protein_(x11)_mrna,_3'_end
25 l09260_781-1171,(chromosome_3p25)_membrane_protein_mrna
l11284_1672-2122_homosapiens_erk_activator_kinase_(mek1)_mrna
l12711_1468-2000,transketolase_(tk)_mrna,_complete_cds
l16991_679-1132,thymidylate_kinase_(cdc8)_mrna,_complete_cds_
l25286_4549-5081,alpha-1_type_xv_collagen_mrna,_complete_cds
30 l32976_2969-3533,protein_kinase_(mlk-3)_mrna,_complete_cds_
l36529mrna_1491-2043,(clone_n5-4)_protein_p84_mrna,_complete_cds_
l36983mrna_3012-3546,dynamin_(dnm)_mrna,_complete_cds_
l37347_1301-1835,integral_membrane_protein_(nramp2)_mrna,_partial
all_m13241_5990-6537,n-myc_gene_exonsand_3_
35 all_m15205_12942-
l3411,thymidine_kinase_gene,_complete_cds,_with_clustered_alu_repeats_in_the_intron
m16707mrna_6-
357,histone_h4_gene,_complete_cds,_clone_fo108,histone_h4_gene,_complete_cds,_clone_fo1
m20747_1519-2034,insulin-responsive_glucose_transporter_(glut4)_mrna,_complete_cds_

- m21121_958-1129,t_cell-specific_protein_(rantes)_mrna,_complete_cds
 m21154mrna_1234-1756,s-adenosylmethionine_decarboxylase_mrna,_complete_cds_
 m23668exon_743-1271,adrenodoxin_gene
 m24470mrna_911-1355,glucose-6-phosphate_dehydrogenase,_complete_cds
5 m25280_1753-2299,lymph_node_homing_receptor_mrna,_complete_cds_
 m28249_4850-5306,very_late_antigen-2_(vla-2)/collagen_receptor_alpha-
 2_subunit_mrna,_complete_cds
 m29536_1025-1361,translational_initiation_factorbeta_subunit_(elf-2-beta)_mrna,_complete_cds
 m34539_1051-1477,fk506-binding_protein_(fkbp)_mrna,_complete_cds_
10 m38591_120-600,cellular_ligand_of_annexin_ii_(p11)_mrna,_complete_cds_
 m54915_2208-2236,h-pim-1_protein_(h-pim-1)_mrna,_complete_cds
 m60091_1118-1248,galactose-1-phosphate_uridyl_transferase_mrna,_complete_cds_
 m60450_1932-2404,voltage-gated_potassium_channel_(hk1)_mrna,_complete_cds
 m60527mrna_1877-2369,deoxycytidine_kinase_mrna,_complete_cds_
15 m63180_2055-2505,threonyl-trna_synthetase_mrna,_complete_cds_
 m69013_1053-1515,guanine_nucleotide-binding_regulatory_protein_(g-y-
 alpha)_mrna,_complete_cds
 m69039_625-1171,pre-mrna_splicing_factor_sf2p32,_complete_sequence_
 m86852_1041-1557,peroxisome_assembly_factor-1_mrna,_complete_cds_
20 m87339_875-1361,replication_factor_37-kda_subunit_mrna,_complete_cds
 m87434_2316-2862,71_kda_2'_5'_oligoadenylate_synthetase_(p69_2-
 5a_synthetase)_mrna,_complete_cds_
 s77356_3-
 41,_transcript_ch21=oligomycin_sensitivity_conferral_protein_oscp_homolog_[human,_rf1,rf48_
25 s78187_2548-3064,_cdc25hu2=cdc25+_homolog_[human,_mrna,_3118_nt]
 u04810_2050-2536,tastin_mrna,_complete_cds_
 u05681exon#7_111-544,proto-oncogene_bcl3_gene
 u10362_848-1352,gp36b_glycoprotein_mrna,_complete_cds
 u14391_4095-4623,myosin-ic_mrna,_complete_cds
30 u15131_3802-4252,p126_(st5)_mma,_complete_cds_
 u20428_2450-2840,snc19_mrna_sequence_
 u24704_790-1264,antisecretory_factor-1_mrna,_complete_cds
 u29607_1974-2148,methionine_aminopeptidase_mrna,_complete_cds
 u34683_1261-1735,glutathione_synthetase_mrna,_complete_cds_
35 u41668_520-976,deoxyguanosine_kinase_mrna,_complete_cds
 u52828_1418-1882,cri-du-chat_region_mrna,_clone_niba2
 u53347_2278-2812,neutral_amino_acid_transporter_b_mrna,_complete_cds_
 u56402_2969-3471,chromatin_structural_protein_homolog_(supt5h)_mrna,_complete_cds
 u58766_741-1299,fx_protein_mrna,_complete_cds

- u59752_524-938,sec7p-like_protein_mrna_partial_cds
u59919_2047-2575,smg_gds-associated_protein_smap_mrna_complete_cds
u60325_3700-
4252,dna_polymerase_gamma_mrna_nuclear_gene_encoding_mitochondrial_protein_complete_cd
- 5** u62293mrna_2576-3152,limk1_gene_(lim-kinase1)_extracted_fromlim-
kinase1_and_alternatively_spliced_1
u69127_2758-3106,fuse_binding_protein(fbp3)_mrna_partial_cds_
u71374_617-1157,hspex13p_mrna_complete_cds/gb=u71374_/ntype=rna_
all_u73167_4971-
- 10** 35099_h_luca14.2a_gene_extracted_fromcosmid_luca14_h_luca14.2a_gene_extracted_from
u83463_1406-1862,scaffold_protein_pbp1_mrna_complete_cds
u86070_629-1205,phosphomannomutase_mrna_complete_cds
u87269_1976-2468,p120e4f_transcription_factor_mrna_complete_cds.
u91985_1014-1320,dna_fragmentation_factor-45_mrna_complete_cds
- 15** u94319_2044-2404,autoantigen_dfs70_mrna_partial_cds.
all_x03794_570-1150,embryonic_mrna_3'_end_with_homoeo_box_(clone_hhoc10)_
all_x05299_2010-2572,mrna_(~95%)_for_major_centromere_autoantigen_cenp-b_
all_x06389_1582-2087,mrna_for_synaptophysin_(p38)
all_x07695_1175-1722,mrna_for_cytokeratinc-terminal_region
- 20** all_x15331_813-1194,mrna_for_phosphoribosylpyrophosphate_synthetase_subunit_one
x15722cds_931-1411:in_reversesequence,_1569-1575,mrna_for_glutathione_reductase_(ec_1.6.4.2)
x15822cds_18-222:in_reversesequence,_13-379,cox_vii-a-1_mrna_for_liver-
specific_cytochrome_c_oxidase_
x17620mrna_257-
- 25** 677,mrna_for_nm23_protein_involved_in_developmental_regulation_(homologto_drosophila
x54637cds_3359-3539:in_reversesequence,_3857-4133,tyk2_mrna_for_non-
receptor_protein_tyrosine_kinase
all_x59727_3618-4201,63_kda_protein_kinase_related_to_rat_erk3_
x63417cds_170-524:in_reversesequence,_560,irlb_mrna_
30 all_x63522_1800-1997,mrna_daudi6_for_retinoic_acid_x_receptor_b
x63657mrna_1683-2169,fvt1_mrna_
x63679cds_587-1073,mrna_for_tramp_protein
all_x69115_718-998,znf37a_mrna_for_zinc_finger_protein_
x71129cds_213-705,mrna_for_electron_transfer_flavoprotein_beta_subunit_
35 x74330cds_788-1154:in_reversesequence,_1281-1335,mrna_for_dna_primase_(subunit_p48)_
x74801cds_1282-1552:in_reversesequence,_1636-1837,cctg_mrna_for_chaperonin
x74874mrna_5857-
6262_rna_polymerase_ii_largest_subunit_gene_extracted_fromgene_for_rna_pol_ii_large
x78992cds_1349-1373,erf-2_mrna_

- all_x80910_3085-3566,ppp1cb_mrna_
x81788_397-799,ds-1_mrna_
x92720cds_1540-1888:in_reversesequence,_1978-
2086,mrna_for_phosphoenolpyruvate_carboxykinase
- 5** x93510cds_548-956:in_reversesequence,_1021-1069,mrna_for_37_kda_lim_domain_protein
x97544cds_291-453:in_reversesequence,_508-724,mrna_for_tim17_preprotein_translocase_
x98248mrna_3140-3698,mrna_for_sortilin
x98534exon#10_287-798,vasp_gene,_exonsto_13_
x99947_2580-2922:in_reversesequence,_2994-3084,mrna_dynein-related_protein
- 10** y00636cds_586-688:in_reversesequence,_739-
985,mrna_for_lymphocyte_function_associated_antigen-3_(lfa
all_y11681_529-1040,mrna_for_mitochondrial_ribosomal_protein_s12/gb=y11681/_ntype=rna_
z23064_1461-1755,mrna_gene_for_hnmp_g_protein_
all_z48042_2679-3232,mrna_encoding_gpi-anchored_protein_p137_
- 15** all_z70219_4-188,mrna_for_5'utr_for_unknown_protein_(clone_icrfp507c0696)
z84497cds_1915-2230:in_fullsequence,_18383-
18624,dna_sequence_from_cosmid_o14_on_chromosomecontains_
- Metagene 388
- 20** d38128exon_604-1126,ip_gene_for_prostacyclin_receptor
d43638_2961-3393,mrna_for_mtg8a_protein_complete_cds
hg2167-ht2237_at_hg2167-ht2237_protein_kinase_ht31,_camp-dependent_
hg2715-ht2811_at_hg2715-ht2811_tyrosine_kinase_
- 25** hg3492-ht3686_at_hg3492-ht3686_uncoupling_protein_ucp
l11373_4183-4609,protocadherin_43_mrna_complete_cds_for_abbreviated_pc43
l34409_624-990,(clone_b3b3e13)_chromosome_4p16.3_dna_fragment_
l36645mrna_2716-3034,receptor_protein-tyrosine_kinase_(hek8)_mrna_complete_cds_
m16801mrna_5250-5724,mineralocorticoid_receptor_mrna_(hmr)_complete_cds_
- 30** m60556mrna#1_503-839,_tgfb3_gene_(transforming_growth_factor-
beta_3)_extracted_fromtransforming_grow
m74096_1694-2096,long_chain_acyl-coa_dehydrogenase_(acadi)_mrna_complete_cds
m97676_1406-1646,(region_7)_homeobox_protein_(hox7)_mrna_complete_cds
s73840_408-
- 35** 784,_type_iix_myosin_heavy_chain_{3'_region}_[human,_skeletal_muscle,_mrna_partial,_827_n
s81661_588-1164,_keratinocyte_growth_factor_[human,_mrna,_1200_nt]
u02683_2758-3318,alpha_palindromic_binding_protein_mrna_complete_cds
u08096exon_31-481,peripheral_myelin_protein-22_(pmp22)_gene,_non-
coding_exon_1b/gb=u08096/_ntype=dna

u37122_1877-2387,adducin_gamma_subunit_mrna,_complete_cds
 u44754_809-1253,pse-binding_factor_ptf_gamma_subunit_mrna,_complete_cds
 u69546_1903-2299,rna_binding_protein_etr-3_mrna,_complete_cds
 u79251_1285-1747,clone_23878_mrna_sequence_
5 all_x04325_1113-1558,liver_mrna_for_gap_junction_protein_
 all_x59350_2679-3220,mrna_for_b_cell_membrane_protein_cd22_
 x67697cds_1-145:in_reversesequence,_63-603,he2_mrna_

Metagene 378

10

d87011cds_1308-1590:in_fullsequence,_24060-
 24222,(lamuda)_dna_for_immunoglobulin_light_chain_
 j04156mrna_1030-1510,interleukin(il-7)_mrna,_complete_cds_
 s95936_1806-2268,_transferrin_[human,_liver,_mrna,_2347_nt]_
15 u24153_1796-1994,p21-activated_protein_kinase_(pak2)_gene,_complete_cds

Metagene 359

20

d86975_5570-5978,mrna_for_kiaa0222_gene,_complete_cds
 105514cds_20-116:in_reversesequence,_1789-1815:not_in_gb_record,histatin(his2)_gene_
 all_x83857_1431-1809,mrna_for_prostaglandin_e_receptor_(ep3a1)_

Metagene 261

25

hg274-ht274_s_at_hg274-ht274_gamma-glutamyltransferase
 u49379_2051-2537,diacylglycerol_kinase_epsilon_dgk_mrna,_complete_cds
 u81607_6007-6535,gravin_mrna,_complete_cds_
 all_x81479_2655-3118,mrna_for_emr1_hormone_receptor
 x86816mrna_4-193,estrogen_receptor_cdna,_5'_splice_variant/gb=x86816/_ntype=rna

30

Metagene 234

35

u50822mrna_909-1375,neurogenic_helix-loop-helix_protein_neurod_(neurod)_gene,_complete_cds
 u68030_2365-2665,g_protein-coupled_receptor_(strl22)_mrna,_complete_cds
 all_u77827_1053-1630,orphan_g_protein-coupled_receptor_(cepr)_gene,_complete_cds.
 all_x77366_4160-4689,hbz17_mrna

Metagene 227

- aj001047cds_485-791:in_reversesequence, 959-1013,mrna_for_matrilin-3/gb=aj001047/_ntype=rna
d25216_4968-5256,mrna_for_kiaa0014_gene,_complete_cds
d29012_230-752,mrna_for_proteasome_subunit_y,_complete_cds_
d29954_4458-4920,mrna_for_kiaa0056_gene,_partial_cds_
5 d45906_3097-3613,mrna_for_limk-2,_complete_cds_
d50810_3494-3992,mrna_for_placental_leucine_aminopeptidase,_complete_cds_
d50913_1494-2052,mrna_for_kiaa0123_gene,_partial_cds_
d63160exon_6-306:in_reversesequence, 9:not_in_gb_record,dna_for_lectin_p35_
d83703_2605-3169,mrna_for_peroxisome_assembly_factor-2,_complete_cds_
10 d90042_675-1215,liver_arylamine_n-acetyltransferase(ec_2.3.1.5)_gene
hg2036-ht2090_at_hg2036-ht2090_stimulatory_gdp/gtp_exchange_protein_for_c-ki-
ras_p21_and_smg_p21_
hg2566-ht4867_at_hg2566-ht4867_microtubule-associated_protein_tau,_altsplice_5,_exon_4a
hg2706-ht2802_at_hg2706-ht2802_serine/threonine_kinase_
15 hg3976-ht4246_at_hg3976-ht4246_pou-domain_dna_binding_factor_pit1,_pituitary-specific
hg870-ht870_at_hg870-ht870_golgin,_165_kda_polypeptide_
hg909-ht909_at_hg909-ht909_mg81
j02876mrna_616-1180,placental_folate_binding_protein_mrna,_complete_cds
105147_266-812,dual_specificity_phosphatase_tyrosine/serine_mrna,_complete_cds_
20 110405_1364-
1910,dna_binding_protein_for_surfactant_protein_b_mrna,_complete_cds/gb=110405/_ntype=rn
114754_3369-3813,dna-binding_protein(smbp2)_mrna,_complete_cds
119058_2599-3163,glutamate_receptor(glur5)_mrna,_complete_cds_
126494_1598-2084,(oct-6)_mrna,_complete_cds_
25 l29433exon_53-587,factor_x(blood_coagulation_factor)_gene_
l36861exon#4_247-757,guanylate_cyclase_activating_protein(gcaph1)_gene_exons_1-
4,_complete_cds_
all_l36922_938-1125,met-ase_gene,_exon_1
l40377mrna_766-1276,cytoplasmic_antiproteinase(cap2)_mrna,_complete_cds
30 l47738_2286-2856,inducible_protein_mrna,_complete_cds_
all_m16652_714-
760,pancreatic_elastase_ii_mrna,_complete_cds,pancreatic_elastase_ii_mrna,_complete
m31651cds_900-1146:in_reversesequence, 5912-6098,human_sex_hormone-
binding_globulin(shbg)_gene,_com
35 all_m34041_1414-2015,alpha-2-adrenergic_receptor(alpha-2_c2)_gene,_complete_cds_
m35878exon#4_1993-2443,insulin-like_growth_factor-binding_protein-
3_gene,_complete_cds,_clone_hl1006
all_m58378_75-406:in_m58378cds#1_1893-
1930:in_m58378cds#2_2002,syn1_gene(synapsin_i)_extracted_fro

- m64595mrna_216-648,small_g_protein_(gx)_mrna,_3'_end_
m76180_1461-1887,aromatic_amino_acid_decarboxylase_(ddc)_mrna,_complete_cds
m86757_2-372,psoriasin_mrna,_complete_cds
m91438cds_55-181:in_reversesequence,_300-540,kazal-type_serine_proteinase_(husi-
5 ii)_gene,_complete_c
m93718_3536-4034,nitric_oxide_synthase_mrna,_complete_cds
m94077exon#2_657-1125,loricrin_gene_exonsand_2,_complete_cds
m94547mrna_55-565,_hummlc2at;_homo_sapiens;_:_593_base-pairs
m95712_2005-2407,b-raf_mrna,_complete_cds
10 m98045_1593-2097,folylpolyglutamate_synthetase_mrna,_complete_cds_
all_s57887_739-
980,(t1)=elastin_translocation_allele_{exon_28,_translocation}_[human,_genomic_mutan
s67070_55-
421,_heat_shock_protein_hsp72_homolog_[human,_thyroid_associated_opthalmopathy_patient,_m
15 s82198_323-827,_caldecrin=serum_calcium-
decreasing_factor_[human,_pancreas,_mrna_partial,_894_nt]
u06088exon_220-730,n-acetylgalactosamine_6-sulphatase_(galns)_gene_
u08191_4687-5220,r_kappa_b_mrna,_complete_cds
u09850_3337-3769,zinc_finger_protein_(znf143)_mrna,_complete_cds_
20 u13045_2126-2690,nuclear_respiratory_factor-2_subunit_betamrna,_complete_cds
all_u15177_2291-2724,cosmid_cri-jc2015_at_d10s289_in_10sp13
u22526_2677-3157,2,3-oxidosqualene-lanosterol_cyclase_mrna,_complete_cds_
u35234_6175-6290,protein_tyrosine_phosphatase_sigma_mrna,_complete_cds_
u41763_4933-5485,muscle_specific_clathrin_heavy_chain_(cltd)_mrna,_complete_cds
25 u42412_977-1535,5'-amp-activated_protein_kinase,_gamma-1_subunit_mrna,_complete_cds_
u48408_752-1322,kidney_water_channel_(hkid)_mrna,_complete_cds_
u49260_1284-1761,mevalonate_pyrophosphate_decarboxylase_(mpd)_mrna,_complete_cds_
u49395_1361-1907,ionotropic_atp_receptor_p2x5a_mrna,_complete_cds
u52112mrna#5_896-
30 1340,xq28_genomic_dna_in_the_region_of_the_11cam_locus_containing_the_genes_for_neu
u55258cds_3452-3872:in_reversesequence,_4031-4091,hbravo/nr-cam_precursor_(hbravo/nr-
cam)_gene,_comp
all_u57341_2-
129,neurofilament_triplet_1_protein_mrna,_partial_cds/gb=u57341/_ntype=ma,neurofilamen
35 u60666_1923-2415,testis_specific_leucine_rich_repeat_protein_(tslrp),_complete_cds_
u65402cds_651-915:in_reversesequence,_1437-1647,seven_transmembrane_g-
coupled_receptor_(gpr31)_gene,
u68485_1356-1788:not_in_gb_record,box-dependent_myc-interacting_protein-
1_(bin1)_mrna,_complete_cds_

- u70064_6458-7030,lysosomal_trafficking_regulator_(lyst)_mrna,_partial_cds_
u72209_432-990,yy1-associated_factor(yaf2)_mrna,_complete_cds_
u87964_1515-2094,putative_g-protein_(gp-1)_mrna,_complete_cds
x00090cds_6-356,histone_h3_gene
- 5** all_x00695_6073-6372,interleukin-2_(il-2)_gene_and_5'-flanking_region_
x01715cds_1338-
1537:not_in_gb_record,gene_fragment_for_the_acetylcholine_receptor_gamma_subunit_prec
x05360cds_353-785,cdc2_gene_involved_in_cell_cycle_control_
all_x13810_1940-1986,otf-2_mrna_for_lymphoid-specific_transcription_factor_
10 x51952mrna_355-
517,_ucp_fromucp_gene_for_uncoupling_protein_exonsand/gb=x51952_/ntype=dna_/annot=exo
all_x63717_1962-2473,mrna_for_apo-1_cell_surface_antigen_
x66839cds_909-1335:in_reversesequence,_1407-1491,matu_mn_mrna_for_p54/58n_protein_
x69950exon#1_1485-2039,dna_sequence_for_wilms'_tumor_gene
- 15** all_x70297_1563-2020,mrna_for_neuronal_nicotinic_acetylcholine_receptor_alpha-7_subunit
x77777_2210-2771,intestinal_vip_receptor_related_protein_mrna
all_x96969_1470-1759,mrna_for_urea_transporter_
x99656cds_798-1068:in_reversesequence,_1251-
1329,mrna_for_protein_containing_sh3_domain,_sh3gl1_
20 reverse_y10871_4016-4220,twist_gene
z25884cds_2453-2897:in_reversesequence,_3062-3068,mrna_for_clc-
1_muscle_chloride_channel_protein
z48475cds_1531-1795:in_reversesequence,_1918-2128,gckr_mrna_for_glucokinase_regulator_
all_z69720_14484-
25 15067,dna_sequence_from_cosmid_ra36_from_a_contig_from_the_tip_of_the_short_arm_of
all_z70220_31-266,mrna_for_5'utr_for_unknown_protein_(clone_icrfp507o0882).
reverse_z95624_34190-
34542,dna_sequence_from_cosmid_u237h1_contains_ras_like_gtpase_and_ests.
- 30** Metagene 217

d17793_633-1161,mrna_for_kiaa0119_gene,_complete_cds_
hg64-ht64_at_hg64-ht64_nf-kappa_b-binding_protein_kbp-1
k03474exon#5_562-829:in_reversesequence,_2817-
35 2919,mullerian_inhibiting_substance_gene,_complete_cds
100022cds_1249-1679:in_reversesequence,_1750-1816,ig_active_epsilon1_5'_ut_v-d-
j_region_subgroup_vh
m31774_1858-2392,thyrotropin_receptor_(tsh)_mrna,_complete_cds_
u58033_24-366,myotubularin_related_protein(mtmr2)_gene,_partial_cds/gb=u58033_/ntype=rna

x06290cds_13307-13442:in_reversesequence,_13709-13913,mrna_for_apolipoprotein(a)_
 x87843cds_690-894:in_reversesequence,_1045-1201,mrna_for_cyclin_h_assembly_factor_
 x99350mrna_1863-2424,_hfh4_cds_gene_extracted_fromhfh4_gene,_exonand_joined_cds

5 Metagene 66

d49824_945-1110,hla-b_null_allele_mrna,hla-b_null_allele_mrna_
 hg862-ht862_s_at_hg862-ht862_transition_protein_
 j04040mrna_563-1016,glucagon_mrna,_complete_cds

- 10 m15881_1752-2310,uromodulin_(tamm-horsfall_glycoprotein)_mrna,_complete_cds
 u77970_2339-2855,neuronal_pas2_(npas2)_mrna,_complete_cds
 x67318cds_851-1229:in_reversesequence,_1260,mrna_for_procarboxypeptidase_a1_

Metagene 60

15

u31382_69-621,g_protein_gamma-4_subunit_mrna,_complete_cds_
 x07820cds_1252-1378:in_reversesequence,_1430-1694,mrna_for_metalloproteinase_stromelysin-2
 x14329cds_1050-1350:in_reversesequence,_1569-
 1641,mrna_for_carboxypeptidase_n_small_subunit_(ec_3.4.

20

z47043cds_540-
 1080,partial_cdna_sequence,_clone_x529,_unknown_open_reading_frame;/gb=z47043/_ntype=d

Metagene 48

25

d26561cds#2_153-435:in_reversesequence,_3711-
 3717,_orf_for_1l_protein_gene_extracted_frompapillomavi
 hg3703-ht3915_s_at_hg3703-ht3915_udp-
 glucuronosyltransferasefamily,_polypeptide_1,_altsplice_1
 all_137868_3521-4088,pou-domain_transcription_factor_(n-oct-3),_complete_cds

30

x74819cds_509-809:in_reversesequence,_913-1015,mrna_for_cardiac_troponin_t

Metagene 21

35

af012270_815-1325,peropsin_(rrh)_mrna,_complete_cds/gb=af012270/_ntype=ma
 l40411mrna_43-511,thyroid_receptor_interactor_(trip8)_mrna,_3'_end_of_cds_
 all_x64877_494-529,mrna_for_serum_protein,mrna_for_serum_protein

Metagene 17

- d50931_2527-2971,mrna_for_kiaa0141_gene,_complete_cds
 m97016_1231-1803,osteogenic_protein-2_(op-2)_mrna,_complete_cds.
 s58544_1884-2382,_75_kda_infertility-
 related_sperm_protein_[human,_testis,_mrna_partial,_2427_nt]_
- 5 s81737_1159-1681,_alphasyntrophin_[human,_mrna_partial,_1771_nt]_
- u06233_2545-3055,pou_domain_protein_(brn-3b)_mrna,_complete_cds
 u07681_2075-2585,nad(h)-
 specific_isocitrate_dehydrogenase_alpha_subunit_precursor_mrna,_complete_cds
 u68385_1259-1643,meis1-related_protein(mrg2),_mrna,_partial_cds.
- 10 u69108_2155-2632,tnf_receptor_associated_factor_mrna,_partial_cds_
- all_x79066_390-973,_hsapiens_erf-1_mrna_5'_end
 x91653_exon_5-125,dna_for_exon_encoding_for_n-
 acetylglucosaminyltransferase_v_(340_bp)/gb=x91653_/nty
 y00083_cds_902-1201:in_reverse_sequence,_1416-1641,mrna_for_glioblastoma-derived_t-
- 15 cell_suppressor_fac

Metagene 478

- k02402_exon#8_1383-1875,coagulation_factor_ix_gene,_complete_cds
- 20 l41162_1879-2419,collagen_alphatype_ix_(col9a3)_mrna,_complete_cds_
- all_m21388_2-95,unproductively_rearranged_ig_mu-chain_mrna_v-region_(vd),_5'_end,_clone_mu-
 3a1a,unp
 all_m29610_446-476,glycophorin_e_mrna,_complete_cds,glycophorin_e_mrna,_complete_cds
 u79286_934-1294,arginine_methyltransferase_mrna,_complete_cds

25

Metagene 313

- ac002045_mrna#1_643-838,_a-589h1.1_from_chromosome_bac_clone_cit987-ska-
 589h1_~complete_genomic_sequenc
- 30 aj000099_1243-1750,mrna_for_lyosomal_hyaluronidase/gb=aj000099_/ntype=rna
- d83260_604-1150,hxc-26_mrna,_complete_cds
 j04823_mrna_61-391,cytochrome_c_oxidase_subunit_viii_(cox8)_mrna,_complete_cds_
- l11066_2272-2770,mrna_sequence_
- l13939_3297-3791,beta_adaptin_protein_mrna,_complete_cds_
- 35 l25878_1092-1657,p33/heh_epoxide_hydrolase_(ephx)_mrna,_complete_cds
- m34668_3044-3590,protein_tyrosine_phosphatase_(ptpase-alpha)_mrna
 m64929_1572-2100,protein_phosphatase_2a_alpha_subunit_mrna,_complete_cds_
- m74491_3066-3552,adp-ribosylation_factor_mrna,_complete_cds
 m88279_1591-2131,immunophilin_(fkbp52)_mrna,_complete_cds

- m94046_1788-2346,zinc_finger_protein_(maz)_mrna
s82470_1398-1836,bb1=malignant_cell_expression-enhanced_gene/tumor_progression-enhanced_gene_[human]
u04241_979-1264,homolog_of_drosophila_enhancer_of_split_m9/m10_mrna_complete_cds
- 5** u13991_335-713,tata-
binding_protein_associated_factor_30_kda_subunit_(tafi30)_mrna_complete_cds
u18937_1840-2344,histidyl-trna_synthetase_homolog_(ho3)_mrna_complete_cds_
u32986_3609-4126,xeroderma_pigmentosum_group_e_uv-damaged_dna_binding_factor_mrna_complete_cds
- 10** u37146_5411-
5927,silencing_mediator_of_retinoid_and_thyroid_hormone_action_(smrt)_mrna_complete_cds
u41635_2207-2651,os-9_precucosor_mrna_complete_cds
u60644_1537-1957,hu-k4_mrna_complete_cds
u65579_138-648,mitochondrial_nadh_dehydrogenase-ubiquinone_fe-
- 15** s_protein_8_23_kda_subunit_precursor_
u67171_229-697,selenoprotein_w_(selw)_mrna_complete_cds/gb=u67171_/ntype=rna
u78735_5872-6424,abc3_mrna_complete_cds.
u79287_813-1305,clone_23867_mrna_sequence
u82108_987-1464,sip-1_mrna_complete_cds_
- 20** u83246_1364-1904,copine_i_mrna_complete_cds_
u95040_2366-2876,transcriptional_corepressor_hkap1/tif1b_mrna_complete_cds
all_x04106_907-1478,mrna_for_calcium_dependent_protease_(small_subunit)
x57346cds_308-674:in_reversesequence,1118-1154,mrna_for_hsl_protein
x70649_2231-2663,cl.1042_mrna_of_dead_box_protein_family_
- 25** all_x72964_606-1027,mrna_for_caltractin
all_x73358_355-815,haes-1_mrna_
x92896exon#2-3_39-222:in_reversesequence,295-301,mrna_for_itba2_protein
x98801cds_3489-3729:in_reversesequence,3771-4017,mrna_for_dynactin_
x99728exon_13-247,ndufv3_gene_exon/gb=x99728_/ntype=dna_/annot=exon
- 30** y07604cds_291-483:in_reversesequence,572-776,mrna_for_nucleoside-diphosphate_kinase_
z14244cds_31-169:in_reversesequence,43-
409,coxviib_mrna_for_cytochrome_c_oxidase_subunit_viiB
z56281cds_772-1222:in_reversesequence,1334-1382,mrna_for_interferon_regulatory_factor_3
all_z69881_3952-4535,mrna_for_adenosine_triphosphatase_calcium
- 35** Metagene 207
- hg2160-ht2230_at_hg2160-ht2230_glutamate_decarboxylase
u68723_2126-2576,checkpoint_suppressormrna_complete_cds

x76059cds_1208-1424:in_reversesequence, 1709-1807,mrna_for_yrrm1

Metagene 206

- 5 m90354cds_29-301:in_reversesequence, 1165-1197,btf3_protein_homologue_gene, complete_cds
u57452_43-103,snf1-like_protein_kinase_mrna, partial_cds/gb=u57452_/ntype=rna
u62432_1759-
1881,nicotinic_acetylcholine_receptor_alpha3_subunit_precursor, mrna, complete_cds_
x87852cds_5374-5560:in_reversesequence, 5780-5966,mrna_for_sex_gene_
10 all_z29678_1247-1740,mitf_mrna_

Metagene 62

- u07132_1415-1961,steroid_hormone_receptor_ner-i_mrna, complete_cds_
15 x99374cds_1846-2174:in_reversesequence, 2211-2318,mrna_for_fertilin_beta

Metagene 387

- ab002409_293-791,mrna_for_slc, complete_cds/gb=ab002409_/ntype=rna
20 af009368_901-1345,luman_mrna, complete_cds/gb=af009368_/ntype=rna_
d11327_2099-2638,mrna_for_protein-tyrosine_phosphatase, complete_cds_
d16827cds_767-1064:in_reversesequence, 1124-
1132, gene_for_fifth_somatostatin_receptor_subtype_
d17461exon#1-3_13-102: not_in_gb_record, gulo_gene_for_l-gulono-gamma-
25 lactone_oxidase, exon_9,10_and/g
d21089_2957-3515,mrna_for_xp-c_repair_complementing_protein(p125), complete_cds_
d31891_3786-4275,mrna_for_kiaa0067_gene, complete_cds
d32002_2454-3001,mrna_for_nuclear_cap_binding_protein, complete_cds
d42053_3755-4277,mrna_for_kiaa0091_gene, complete_cds
30 d50312_1206-1668,mrna_for_ukatp-1, complete_cds
d63485_2710-3196,mrna_for_kiaa0151_gene, complete_cds
d85939_746-1037,mrna_for_p97_homologous_protein, complete_cds
d87012cds_1986-2226:in_fullsequence, 34522-34687,(lambda)_dna_for_immunoglobulin_light_chain
d87432_5731-6253,mrna_for_kiaa0245_gene, complete_cds
35 d90279_5154-5590,mrna_for_collagen_alpha_1(v)_chain, complete_cds
hg2442-ht2538_at_hg2442-
ht2538_tropomyosin, alpha, muscle, altsplice_2, skeletal_muscle_(fibroblast)
hg2686-ht2782_at_hg2686-ht2782_ryanodine_receptor_

- hg2992-ht5186_at_hg2992-ht5186_beta-
 hexosaminidase, alpha polypeptide, abnormal splice mutation
 hg3175-ht3352_at_hg3175-ht3352_carcinoembryonic_antigen
 hg3254-ht3431_at_hg3254-ht3431_phosphatidylinositol_3-kinase_p110, beta isoform
- 5** j00220_cds4_at_j00220_j00220,not_in_gb_record,ig_germline_h-chain_g-e-a_region_a: gamma-3_5' flank,i
 j02854_531-1089,20-kda_myosin_light_chain_(mlc-2)_mrna, complete_cds_
 j03810_2627-3113,liver_glucose_transporter-like_protein_(glut2), complete_cds
 all_k03430_414-853,complement_c1q_b-chain_gene_
- 10** 104751_1994-2510,cytochrome_p-450_4a_(cyp4a)_mrna, complete_cds
 110378_1130-1640,(clone_ctg-b43a)_mrna_sequence
 110955cds#1_184-560:in_reversesequence, 394-
 467, carbonic_anhydrase_iv_gene_extracted_fromcarbonic_a
 111369_756-1296,protocadherin_42_mrna, 3' end_of_cds_for_alternative_splicing_pc42-8_
- 15** all_111672_3552-
 3579,kruppel_related_zinc_finger_protein_(htf10)_mrna, complete_cds,kruppel_related_
 113329exon_434-938,iduronate-2-sulfatase_(ids)_gene_
 114565exon#9_5-359,peripherin_(prph)_gene_exons_1-9, complete_cds
 115409_1227-1719,(clone_g7)_von_hippel-lindau_disease_tumor_suppressor_mrna_sequence
- 20** 120815_2031-2445,s_protein_mrna, complete_cds
 129376_616-1126,(clone_3.8-1)_mhc_i_mrna_fragment_
 133930_1504-2054,cd24_signal_transducer_mrna, complete_cds_and_3'_region
 142324cds_530-944,(clone_gpcr_w)_g_protein-
 linked_receptor_gene_(gpcr)_gene, 5' end_of_cds/gb=142324
- 25** 142450mrna_1022-1448,pyruvate_dehydrogenase_kinase_isoenzyme(pdk1)_mrna, complete_cds
 147125mrna_1504-2055,(chromosome_x)_glypican_(gpc3)_mrna, complete_cds
 148211cds_31-151:in_reversesequence, 1691-1775,angiotensin_ii_receptor_gene, complete_cds
 149173cds_13-116,ocp2_gene, partial_cds/gb=149173/_ntype=dna/_annot=cds
 m14539_3238-3730, factor_xiii_subunit_a_mrna, 3' end
- 30** m19507mrna#4_2620-3184,myeloperoxidase_mrna, complete_cds
 m20778_401-974, homo_sapien, alpha-3_(vi)_collagen
 m20786exon_630-1146,alpha-2-plasmin_inhibitor_gene_
 all_m21494_152-645:in_m21494cds_888-967,muscle_creatine_kinase_gene_(ckmm), 5' flank
 all_m22919_3226-3665, _mlc_gene_(non-
- 35** muscle_myosin_light_chain)_extracted_fromnonmuscle/smooth_muscle
 m37755exon_15-256:in_reversesequence, 280-453:not_in_gb_record, pregnancy-specific_beta-1-
 glycoprotei
 m58583_989-1487,precerebellin_and_cerebellin_mrna, complete_cds
 m64347_3336-3720,novel_growth_factor_receptor_mrna, 3' cds_

- m74297_1161-1551,homeobox_1.4_protein_mrna,_complete_cds_
m75106_1138-1618,prepro-plasma_carboxypeptidase_b_mrna,_complete_cds_
m77810_2324-2585,transcription_factor_gata-2_(gata-2)_mrna,_complete_cds_
m82827mrna_2078-2228,fusion_protein_mrna,_complete_cds.
- 5** m91467_1375-1861,serotonin_receptor_(5ht1e)_mrna,_complete_cds_
m95929_1015-1399,homeobox_protein_(phox1)_mrna,_3'_end_
s76638_2553-3003,p50-nf-
kappa_b_homolog_[human,_peripheral_blood_t_cells,_mrna,_3113_nt]_
s82240_274-802,_rho=26_kda_gtpase_homolog_[human,_hela_cell_line,_mrna,_833_nt] .
- 10** u03090_457-955,ca2+-dependent_phospholipase_a2_mrna,_complete_cds
all_u04325_3581-3780,_psg11_gene_(pregnancy-specific_beta-1-glycoproteinc-
a_domain)_extracted_frompr
u07969_2956-3259,intestinal_peptide-associated_transporter_hpt-1_mrna,_complete_cds
u08438exon#15_1106-1571,beta-adrenergic_receptor_kinase_(adrbk1)_gene
- 15** u17034_4182-4584,soluble_pla2_receptor_mrna,_complete_cds
u18550exon_1402-1954,gpr3_g_protein-coupled_receptor_gene,_complete_cds
u22961_2627-3194,mrna_clone_with_similarity_to_l-glycerol-3-
phosphate:nad_oxidoreductase_and_albumin
u24685cds_123-336:in_reversesequence,_420-447,anti-
- 20** b_cell_autoantibody_igm_heavy_chain_variable_v-d-
u40152_2541-3103,origin_recognition_complex(hsorc1)_mrna,_complete_cds
u55766_535-1081,rev_interacting_protein_rip-1_mrna,_complete_cds_
u64805_1668-2218,brca1-delta11b_(brca1)_mrna,_complete_cds/gb=u64805_/ntype=rna
u65011_1625-2039,preferentially_expressed_antigen_of_melanoma_(prame)_mrna,_complete_cds.
- 25** u69961_1565-1997,solurshin_(rgs)_mrna,_complete_cds
u70136_4546-4957,megakaryocyte_stimulating_factor_mrna,_complete_cds_
u71598_444-792,zinc_finger_protein_zfp2_(zf2)_mrna,_partial_cds
u88726_55-433,symplekin_mrna,_partial_cds/gb=u88726_/ntype=rna_
u90919_1637-2129,clones_23667_and_23775_zinc_finger_protein_mrna,_complete_cds_
- 30** all_x05276_1466-2031,mrna_for_fibroblast_tropomyosin_tm30_(pl)
all_x05309_4846-5240,mrna_for_c3b/c4b_receptor_(cr1)_f_allotype
x14046cds_479-809:in_reversesequence,_944-1082,mrna_for_leukocyte_antigen_cd37
all_x14362_1961-2370,cr1_mrna_for_c3b/c4b_receptor_secreted_form_
x14675cds_31-163,bcr-abl_mrna_5'_fragment_(clone_3c)/gb=x14675_/ntype=rna
- 35** x55448exon#22_131-683,_g6pd_gene_(glucose-6-
phosphate_dehydrogenase)_extracted_fromg6pd_gene_for_glu
x61373mrna#1_3441-3693:not_in_gb_record,microtubule-'
associated_protein_tau_(tau)_gene,_alternatively
all_x62078_1997-2400,mrna_for_gm2_activator_protein

- x68264mrna_3300-
 3552,_muc18_gene (melanoma associated glycoprotein)_extracted_frommgf_gene_exons_1&2
 x77567cds_853-1215:in_reversesequence,_1354-1518,mrna_for_insp3_5-phosphatase_
 all_x77753_2390-2787,trop-2_gene_
5 all_x83492_418-500,mrna_for_fas/apo-1_(clone_pertm11-
 fasdelta(4,7))/gb=x83492_/ntype=rna,mrna_for_fa
 x85740mrna_1112-1604,mrna_for_c-c_chemokine_receptor-4_
 x87211cds_486-1041,mrna_for_anion_exchange_protein/gb=x87211_/ntype=rna
 all_x90846_2935-3407,mrna_for_mixed_lineage_kinase_2,mrna_for_mixed_lineage_kinase_2
10 x97303mrna_11-93,mrna_for_ptg-12_protein/gb=x97303_/ntype=rna
 x98260cds_1280-1706,mrna_for_m-phase_phosphoprotein,_mpp11_
 y08134cds_1026-1362:in_reversesequence,_1531-1573,mrna_for_asm-like_phosphodiesterase_3b
 all_y08223_2471-2952,mfh-1_gene
 z11518mrna_1546-2066,mrna_for_histidyl-trna_synthetase_
15 z26256exon_64-364,isoformgene_for_l-
 type_calcium_channel,_exon/gb=z26256_/ntype=dna_/annot=exon

 Metagene 482

20 107515_253-790,heterochromatin_protein_homologue_(hpl1)_mrna,_complete_cds
 l36051exon#6_678-1086,thrombopoietin_gene,_complete_cds
 u04811_1931-2375,trophinin_mrna,_complete_cds
 u09646exon_358-874,carnitine_palmitoyltransferase_ii_precursor_(cpt1)_gene_
 u11701_1316-1862,lim-homeobox_domain_protein_(hlh-2)_mrna,_complete_cds
25 u23946_1986-2496,putative_tumor_suppressor_(luca15)_mrna,_complete_cds_
 u42359mrna_1197-
 1217,n33_protein_form(n33)_gene,_exonand_complete_cds/gb=u42359_/ntype=dna_/annot=ex
 u49973cds#2_37-
 367,_orf1;_mer37;_putative_transposase_similar_to_pogo_element_fromtiger1_transposab
30 u79263_995-1535,clone_23760_mrna,_partial_cds
 u86529_584-1130,glutathione_transferase_zeta(gstz1)_mrna,_complete_cds/gb=u86529_/ntype=rna_
 all_x52943_2163-2728,mrna_for_atf-a_transcription_factor_
 x98266cds#2_1028-1340:in_reversesequence,_2103-2223,_ligase-
 like_protein_gene_extracted_frommrna_for
35 z83802_133-511,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc3)

 Metagene 358

 hg2841-ht2970_at_hg2841-ht2970_albumin,_altsplice_5

u12259cds_492-808:in_reversesequence,_16275-16368,paired_box_homeotic_protein_(pax3)_gene
all_y07701_3290-3651,mrna_for_aminopeptidase_

Metagene 305

5

d17357exon_25-295,activin_beta-
a_gene_regulatory_sequence_of_5'_upstream_region/gb=d17357_/ntype=dn
d28124_1346-1886,mrna_for_unknown_product,_complete_cds

d86425_4224-4776,osteoblast_mrna_for_osteonidogen,_complete_cds

10 l12350mrna_5247-5721,thrombospondin(thbs2)_mrna,_complete_cds_

l13923_9109-9601,fibrillin_mrna,_complete_cds_

m12125mrna_671-1013,fibroblast_muscle-type_tropomyosin_mrna,_complete_cds

m83186_103-

316,cytochrome_c_oxidase_subunit_viia_(cox7a)_muscle_isoform_mrna,_complete_cds_

15 m92934mrna_1492-2026,connective_tissue_growth_factor,_complete_cds_

u09278_2285-2735,fibroblast_activation_protein_mrna,_complete_cds

u19718_479-947,microfibril-associated_glycoprotein_(mfap2)_mrna,_complete_cds

u30521_1621-1951,p311_hum_-3.1_mrna,_complete_cds

u89942_2867-3383,lysyl_oxidase-related_protein_(ws9-14)_mrna,_complete_cds_

20 x02419mrna_1754-2210,upa_gene_

x57579exon_545-840:in_reversesequence,_1392-1555,activin_beta-a_subunit_(exon_2)

all_x63759_1241-1752,htnp2_gene_for_transition_protein_2_

Metagene 197

25

ab000114_1818-2208,mrna_for_osteomodulin,_complete_cds_

ab000905_1045-1253,dna_for_h4_histone,_complete_cds

af005043_3474-3990,poly(adp-

ribose)_glycohydrolase_(hparg)_mrna,_complete_cds/gb=af005043_/ntype=rna

30 d42108_4054-4414,mrna_for_phospholipase_complete_cds

d50927_3955-4411,mrna_for_kiaa0137_gene,_complete_cds

all_d87023_19383-19642,_j1_gene_extracted_from(lambda)_dna_for_immunoglobulin_light_chain_

hg3231-ht3408_at_hg3231-ht3408_protease_receptor-1,_effector_cell

l40384mrna_22-487,thyroid_receptor_interactor_(trip13)_mrna,_partial_cds/gb=l40384_/ntype=rna_

35 m60052_2004-2280,histidine-rich_calcium_binding_protein_(hrc)_mrna,_complete_cds_

m60315_2334-2838,transforming_growth_factor-beta_(tgf-beta)_mrna,_complete_cds_

u09368_1908-2298,zinc_finger_protein_znf140

u36621exon_17-536,y-chromosome_rna_recognition_motif_protein_(yrrm)_gene

u47414_1449-1959,cyclin_g2_mrna,_complete_cds

u64198_3571-3955,il-12_receptor_beta2_mrna,_complete_cds_
 y09443_1545-1935,mrna_for_alkyl-dihydroxyacetonephosphate_synthase_precursor_
 all_z17240_956-1014,for_mrna_encoding_hmg2b_

5 Metagene 386

- ab000584_618-1032,mrna_for_tgf-beta_superfamily_protein,_complete_cds_
 ab002366_5112-5616,mrna_for_kiaa0368_gene,_partial_cds/gb=ab002366_/ntype=rna
 ab004884_2491-2995,mrna_for_pku-alpha,_partial_cds/gb=ab004884_/ntype=rna
- 10 d10995cds_828-1128:in_reversesequence,_1245-
 1401,gene_for_serotonin_1b_receptor,_complete_cds_
 d28588_2747-3263,mrna_for_kiaa0048_gene,_complete_cds
 d63813_1154-1676,mrna_for_rod_photoreceptor_protein,_complete_cds
 hg2730-ht2828_s_at_hg2730-ht2828_fibrinogen,_a_alpha_polypeptide,_altsplice_3,_e_
- 15 j05428_1624-1800,3,4-catechol_estrogen_udp-glucuronosyltransferase_mrna,_complete_cds
 l27080cds_538-946:in_reversesequence,_1159-
 1207,melanocortinreceptor_(mc5r)_gene,_complete_cds_
 m34192mrna_1406-1826,isovaleryl-coa_dehydrogenase_(ivd)_mrna,_complete_cds_
 m37075_at_m37075_m37075,not_in_gb_record,embryonic/atrial_myosin_light_chain_(mlc-1-
 20 emb/a_isoform)_g
 m58285_3356-3788,membrane-associated_protein_(hem-1)_mrna,_complete_cds
 m93143_461-499,plasminogen-like_protein_(plgl)_mrna,_complete_cds
 m93415_1865-2303,activin_type_ii_receptor_mrna,_complete_cds_
 m97496_25-409,guanylin_mrna,_complete_cds_
 25 u03858_806-1040,flt3_ligand_mrna,_complete_cds_
 u09579_1537-2041,melanoma_differentiation_associated_(mda-6)_mrna,_complete_cds
 u10690exon#3_934-1499,mage-5b_antigen_(mage5b)_gene,_complete_cds
 u11863_1914-1974,clone_hp-
 dao2_diamine_oxidase,_copper/topa_quinone_containing_mrna,_complete_cds
- 30 u15197_74-363,histo-blood_group_abo_protein_mrna,_partial_3'_utr_sequence
 u17838_7401-7899,zinc_finger_protein_riz_mrna,_complete_cds
 u55853_1917-2433,130_kd_golgi-localized_phosphoprotein_(gpp130)_mrna,_complete_cds
 all_x83127_1494-1624,mrna_for_voltage_gated_potassium_channels,_beta_subunit_
 x95654cds_2682-2862:in_reversesequence,_3022-3202,mrna_for_scpl_protein_
 35 all_x98253_1221-1334,znf183_gene/gb=x98253_/ntype=rna

Metagene 294

a28102cds_986-1442:in_reversesequence,_1546-1582,gabaa_receptor_alpha-3_subunit.

- m17446mrna_648-1186,kaposi_sarcoma_oncogene_fibroblast_growth_factor_mrna_complete_cds
 m98528utr#1_543-1101,neuron-specific_protein_gene_last_exon_clone_d4s234
 u20816mrna#1_258-795,nuclear_factor_kappa-b2_(nf-
 kb2)_gene_partial_cds/gb=u20816/_ntype=dna/_annot=
 5 all_u31799_528-683:in_u31799cds_1746-1777,melanocyte_protein_pm1gene_
 all_x87870_2045-2289,mrna_for_hepatocyte_nuclear_factor_4a_

Metagene 238

- 10 m15856mrna#1_2984-3488,lipoprotein_lipase_mrna_complete_cds_
 m23575_1395-1933,pregnancy-specific_beta-1_glycoprotein_mrna_complete_cds_
 m60503cds_2942-3212:in_reversesequence,_1915-2047,profilaggrin_gene_partial_cds
 s81294_4-
 160,_dcc=deleted_in_colorectal_cancer_{alternatively_spliced,_exon_1a}_[human_brain_tumor,
 15 all_s85963_4324-4544,_hirs-1=rat_insulin_receptor_substrate-
 1_homolog_[human_cell_line_focus_genom

Metagene 200

- 20 m24351exon_248-404,_pthlh_gene(parathyroid_hormone-
 like_protein_a)_extracted_fromparathyroid_hormon
 m31210_2258-2708,endothelial_differentiation_protein_(edg-1)_gene_mrna_complete_cds_
 m55024_2-331,cell_surface_glycoprotein_p3.58_mrna_partial_cds/gb=m55024/_ntype=rna
 m58459_295-829,ribosomal_protein_(rps4y)_isoform_mrna_complete_cds
 25 m60626mrna_1283-1577,n-formylpeptide_receptor_(fnlp-r98)_mrna_complete_cds
 m60724_1847-2321,p70_ribosomal_s6_kinase_alpha-i_mrna_complete_cds
 s72024cds_13-437,_eif-
 5a=eukaryotic_initiation_factor_5a_{clone_cos_9.1}_[human_placenta_genomic,_
 u13695cds_2418-2754:in_reversesequence,_2858-
 30 2954,homolog_of_yeast_mutl_(hpms1)_gene_complete_cds
 u38896_1411-1921,zinc_finger_protein_c2h2-171_mrna_complete_cds_
 x59434mrna_631-1129,rohu_mrna_for_rhodanese
 all_x71661_2263-2768,ergic-53_mrna_
 all_x96586_2898-3343,mrna_for_fan_protein

35

Metagene 364

l31573_1849-2347,sulfite_oxidase_mrna_complete_cds
 m11973_cds1_at_m11973_m11973,not_in_gb_record,gamma-b-crystallin_gene_(gamma_1-2)_

m29474mrna_5986-6490,recombination_activating_protein_(rag-1)_gene,_complete_cds_
u08471_492-780,folate_receptormrna,_complete_cds
u57352_2094-2646,sodium_channel(hbnac1)_mrna,_complete_cds
u76388_1630-1842,steroidogenic_factormrna,_complete_cds_
5 all_z22536_1732-2333,alk-4_mrna,_complete_cds_

Metagene 343

- d25217_2864-3410,mrna_for_kiaa0027_gene,_partial_cds_
10 d45371mrna_4040-4464,apml_mrna_for_gs3109_(novel_adipose_specific_collagen-like_factor),_complete_cd
d85815cds_282-564;in_reversesequence,_753-879,dna_for_rhohp1,_complete_cds
hg1205-ht1205_at_hg1205-ht1205_collagen_type_iv_alpha_2_n-terminus
hg4157-ht4427_at_hg4157-ht4427_glycinamide_ribonucleotide_synthetase_
15 hg732-ht732_at_hg732-ht732_serum_amyloid_a1
j03600_2058-2364,lipoxygenase_mrna,_complete_cds_
k01911mrna_85-481,neuropeptide_y_(npy)_mrna,_complete_cds
l05148_1890-2388,protein_tyrosine_kinase_related_mrna_sequence_
l05779_1535-2069,cytosolic_epoxide_hydrolase_mrna,_complete_cds
20 l10123_3572-4100,surfactant_protein_a_mrna,_complete_cds
l19297_602-1034,nuclear-encoded_mitochondrial_carbonic_anhydrase_(ca5)_mrna,_complete_cds
l29277_2204-2762,dna-binding_protein_(aprf)_mrna,_complete_cds
l38707mrna_2405-2951,diacylglycerol_kinase_(dagk)_mrna,_complete_cds.
l41668_887-1433,udp-galactoseepimerase_(gale)_gene,_complete_cds
25 l48516_473-1013,paraaxonase(pon3)_mrna,_3'_end_of_cds
m13829_603-1029,putative_raf_related_protein_(pks/a-raf)_mrna,_partial_cds_
m14565mrna_1262-1712,cholesterol_side-chain_cleavage_enzyme_p450scc_mrna,_complete_cds_
m20777_434-956,_homo_sapiens,_alpha-2_(vi)_collagen_
m29696_1063-1597,interleukin-7_receptor_(il-7)_mrna,_complete_cds
30 m37271cds_361-672;in_reversesequence,_2722-2909,cd7_antigen_gene,_exons_4-jan_
m54951mrna_438-852,atrial_natriuretic_factor_gene
all_m59829_2774-3117,mhc_iii_hsp70-hom_gene_(hla),_complete_cds
m60298_2117-2615,erythrocyte_membrane_protein_band_4.2_(epb42)_mrna,_complete_cds
m68519mrna_1542-1916,pulmonary_surfactant-associated_protein_sp-
35 a_(sftp1)_gene,_complete_cds
m69197mrna#1_611-1184,_hpr_fromhaptoglobin_and_haptoglobin-related_protein_(hp_and_hpr)_genes,_compl
m74091_925-1453,cyclin_mrna
m80629_1678-2170,cdc2-related_protein_kinase_(ched)_mrna,_complete_cds_

- m89957_675-
 1095,immunoglobulin_superfamily_member_b_cell_receptor_complex_cell_surface_glycoprotein_
 m93405_888-1374,methylmalonate_semialdehyde_dehydrogenase_gene,_complete_cds_
 m93650_1119-1599,paired_box_gene_(pax6)_homologue,_complete_cds
- 5** m99701_627-1137,(pp21)_mrna,_complete_cds_
 s69265_1402-1943,_neuron-specific_rna_recognition_motifs_(rrms)-
 containing_protein_[human,_hippocamp
 s75989_1492-1948,_gamma-
 aminobutyric_acid_transporter_type[human,_fetal_brain,_mrna,_1991_nt]
- 10** s76475_2144-2659,_trkc_[human,_brain,_mrna,_2715_nt]
 u07358_2794-3310,protein_kinase_(zpk)_mrna,_complete_cds_
 u09877_3381-3849,helicase-like_protein_(hlp)_mrna,_complete_cds
 u10991_6267-6789,g2_protein_mrna,_partial_cds
 u16031_2451-2943,transcription_factor_il-4_stat_mrna,_complete_cds_
15 u26398_2628-3168,inositol_polyphosphate_4-phosphatase_mrna,_complete_cds_
 u26403_991-1495,receptor_tyrosine_kinase_ligand_lerk-7_precursor_(eplg7)_mrna,_complete_cds
 u30930_1877-2423,udp-galactose_ceramide_galactosyl_transferase_(cgt)_mrna,_complete_cds
 u43431_3166-3712,dna_topoisomerase_iii_mrna,_complete_cds
 u52840_7503-7755,cri-du-chat_region_mrna,_clone_csa1_
20 u64998cds_61-
 361,ribonuclease_k6_precursor_gene,_complete_cds/gb=u64998_/ntype=dna_/annot=cds
 u82535_1485-2019,fatty_acid_amide_hydrolase_mrna,_complete_cds.
 all_v00565_2218-
 2422,gene_for_preproinsulin,_from_chromosomeincludes_a_highly_polymorphic_region_ups
- 25** x04445mrna_521-1075,inha_gene_exon(and_joined_cds)_
 x06985mrna_943-1393,mrna_for_heme_oxygenase
 x07732mrna#2_991-1543,hepatoma_mrna_for_serine_protease_hepsin_
 all_x52773_1343-1866,mrna_for_retinoic_acid_receptor-like_protein
 x60188mrna_1360-1741,erk1_mrna_for_protein_serine/threonine_kinase_
30 x60957cds_3066-3378:in_reversesequence,_3432-
 3678,tie_mrna_for_putative_receptor_tyrosine_kinase_
 x86779cds_1174-1606:in_reversesequence,_1741,mrna_for_fast_kinase_
 x99961cds_55-409,mrna_for_novel_protein/gb=x99961_/ntype=rna_
 z26317cds_2904-3324:in_reversesequence,_3443-3491,mrna_for_desmoglein_2_
35
- Metagene 174
- d89289_1431-1947,mrna_for_n-acetyl-beta-d-glucosaminide,_complete_cds

105188cds_2-194;in_reversesequence,_281-342,small_proline-
rich_protein(spr2b)_gene,_complete_cds_
m74509_7730-8246,endogenous_retrovirus_type_c_oncovirus_sequence.
s70004_2347-2779,_glycogen_synthase_[human,liver,_mrna,_2912_nt]
5 u65416mrna_1983-2316,mhc_i_molecule_(mich)_gene,_complete_cds_
u79285_892-1402,clone_23828_mrna_sequence

Metagene 171

10 hg1111-ht1111_at_hg1111-ht1111_ras-like_protein_tc21_
k02100mrna_983-1421,ornithine_transcarbamylase_(otc)_mrna,_complete_coding_sequence
u08015mrna_2388-2700,nf-atc_mrna,_complete_cds_
u09413_1957-2389,zinc_finger_protein_znf135_mrna,_complete_cds_
u70862_1029-1248,nuclear_factor_i_b3_mrna,_complete_cds
15 all_x01059_941-
1512,placenta_mrna_for_luteinizing_hormone_releasing_hormone_precursor_(lhrh)_
all_x66436_1427-1980,hsr1_mrna_(partial)_
x80507cds_1020-1314;in_reversesequence,_1624-1828,yap65_mrna_
all_x99141_1411-1715,mrna_for_hair_keratin,_hbb3_

20

Metagene 51

d13988_897-1353,rab_gdi_mrna,_complete_cds_
d31763_5458-5968,mrna_for_kiaa0065_gene,_partial_cds_
25 hg1747-ht1764_s_at_hg1747-ht1764_proto-oncogene_met_altsplice_form_2
hg4074-ht4344_at_hg4074-ht4344_rad2
j05614mrna_4_
41,proliferating_cell_nuclear_antigen_(pcna)_gene,_promoter_region/gb=j05614_/ntype=dna
l23959_971-1415,e2f-related_transcription_factor_(dp-1)_mrna,_complete_cds
30 l40386mrna_657-1122,dp-2_mrna,_complete_cds
l40403mrna_1725-2277,(clone_zap3)_mrna,_3'_end_of_cds_
m28209_158-680,gtp-binding_protein_(rab1)_mrna,_complete_cds
m37104_13-421,mitochondrial_atpase_coupling_factorsubunit_(atp5a)_mrna,_complete_cds
m37583mrna_368-824,histone_(h2a.z)_mrna,_complete_cds
35 m58525_603-933,catechol-o-methyltransferase_(comt)_mrna,_complete_cds_
m81118exon#2_669-1149,alcohol_dehydrogenase_chi_polypeptide_(adh5)_gene
m83738_3328-3883,protein-tyrosine_phosphatase_(ptpase_meg2)_mrna,_complete_cds_
m86737_2236-2776,high_mobility_group_box_(ssrp1)_mrna,_complete_cds_
m92439_4255-4633,leucine-rich_protein_mrna,_complete_cds_

- m94630_832-1027,hnmp-c_like_protein_mrna,_complete_cds_
s83364_19-325,_putative_rab5-interacting_protein_{clone_11-
57}_[human,_hela_cells,_mrna_partial,_366
s85655_435-969,_prohibitin_[human,_mrna,_1043_nt]_
- 5** u25182_350-860,antioxidant_enzyme_aoe37-2_mrna,_complete_cds_
u41387_2693-3263,gu_protein_mrna,_partial_cds
u56833_940-1468,vhl_binding_protein-1_(vbp-1)_mrna,_partial_cds
u57627_4598-5078,fetal_brain_oculocerebrorenal_syndrome_(ocr11)_mrna,_complete_cds_
u65410_961-1459,mad2_(hsmad2)_mrna,_complete_cds_
- 10** u83843_725-1145,hiv-1_nef_interacting_protein_(nip7-1)_mrna,_partial_cds/gb=u83843_/ntype=ma
all_x92396_1999-2480,mrna_for_novel_gene_in_xq28_region
x94754cds_2213-2645:in_reversesequence,_2712-2730,mrna_for_yeast_methionyl-
trna_synthetase_homologue
all_x99585_193-608,mrna_for_smt3b_protein
- 15** Metagene 19
- hg721-ht4827_s_at_hg721-ht4827_placental_protein_14,_endometrial_alphaglobulin,_altsplce_2_
119593mrna_2261-2747:in_reversesequence,_2765-
20 2771,interleukinreceptor_beta_(il8rb)_mrna,_complete_c
s34389_1166-1586,_heme_oxygenase-2_[human,_kidney,_mrna,_1627_nt]_
u19523_2299-2851,gtp_cyclohydrolase_i_mrna,_complete_cds_
all_x05232_1530-1771,mrna_for_stromelysin
x12662mrna_936-1398,arginase_gene_exonand_flanking_regions_(ec_3.5.3.1)_(and_joined_cds)_
25 all_x57809_309-
474,rearranged_immunoglobulin_lambda_light_chain_mrna,rearranged_immunoglobulin_lambd
x72308_419-842,mcp-3_mrna_for_monocyte_chemotactic_protein-3_
y00081cds_293-588:in_reversesequence,_5486-5706,(bsf-
2/il6)_gene_for_b_cell_stimulatory_factor-2
30 y11306mrna_1993-2395,_htcf-4_gene_extracted_frommrna_for_beta_catenin/tcf-4_

Metagene 370

l20971_3698-3992,phosphodiesterase_mrna,_complete_cds_
35 u03272_9619-10081,fibrillin-2_mrna,_complete_cds_
u07802exon#2_2748-3228,tis11d_gene,_complete_cds_
all_x78565_6971-7512,mrna_for_tenascin-c,_7560bp_

Metagene 312

- d31716_4264-4831,mrna_for_gc_box_bindig_protein,_complete_cds
 114430_at_114430_114430,not_in_gb_record,udp-
 glucose_pyrophosphorylase_mrna,_complete_cds_and_flanki
- 5 u26591_1640-
 2108,clone_is10_diabetes_mellitus_type_i_autoantigen_(icap69)_mrna,_complete_cds_
 u33837_13803-14343,glycoprotein_receptor_gp330_precursor,_mrna,_complete_cds_
 u33880mrna_189-
 240,betaintegrin_isoform_d_(itgb1)_gene,_partial_cds/gb=u33880_/ntype=dna_/annot=exon
- 10 u62434_1665-
 1787,nicotinic_acetylcholine_receptor_alpha5_subunit_precursor,_mrna,_complete_cds_
 all_x56199_1025-1614,xist_coding_sequence_a_mrna_(locus_dxs399e)
 x60382mrna_2717-3149,col10a1_gene_for_collagen_(alpha-1_type_x)_
 z48520exon#5_1-98:in_reversesequence,_154-163,xg_mrna_(clone_race6)/gb=z48520_/ntype=ma
- 15 Metagene 114
- hg3928-ht4198_s_at_hg3928-ht4198_surfacant_protein_sp-a1_delta_
 105597cds_729-1071:in_reversesequence,_1307-1499,serotonin_receptor_gene,_complete_cds
- 20 u76189_49-355,extl3_mrna,_partial_cds/gb=u76189_/ntype=ma_
 Metagene 110
- d13705_1151-1722,mrna_for_fatty_acids_omega-hydroxylase_(cytochrome_p-
 450hkv),_complete_cds
- 25 d16105_2703-2979,mrna_for_leukocyte_tyrosine_kinase,_complete_cds
 d83017_2365-2810,mrna_for_nel-related_protein,_complete_cds
 hg2255-ht2344_f_at_hg2255-ht2344_phosphoribosyl_pyrophosphate_synthetase,_subunit_iii
 hg2797-ht2906_s_at_hg2797-ht2906_clathrin_light_polypeptide_altsplice_2
- 30 k03192_566-964,cytochrome_p-450_mrna,_partial
 m13058exon#3_1-372,acidic_proline-rich_protein_(prh2)_gene,_complete_cds_
 m13149_1540-2008,histidine-rich_glycoprotein_mrna,_complete_cds
 all_m29335_62-94,mhc_ii_do-alpha_mrna,_partial_cds,mhc_ii_do-alpha_mrna,_partial_cds
 all_m32879_690-1129,steroid_11-beta-hydroxylase_(cyp11b1)_gene,steroid_11-beta-
- 35 hydroxylase_(cyp11b1)
 m33772mrna_69-631,fast_skeletal_muscle_troponin_c_gene_
 m55513mrna_2274-2767,potassium_channel_(hpcn1)_mrna,_complete_cds
 m62303_726-872,retinoic_acid_receptor-beta_associated_open_reading_frame,_complete_sequence
 m64269cds_389-718:in_reversesequence,_7859-7876,mast_cell_chymase_gene,_complete_cds

- m74587mrna_953-1425,insulin-
like_growth_factor_binding_protein_(higfbp1)_gene,_complete_cds_
m83652_932-1457,complement_component_properdin_mrna,_complete_cds_
s77576_3-
- 5 60,_erv9_reverse_transcriptase_homolog_{clone_rt18}_{human,_multiple_sclerosis,_brain_plaqu
u05012_2204-2720,receptor_tyrosine_kinase_trkc_(ntrk3)_mrna,_complete_cds
u11862_1844-2402,clone_hp-dao1_diamine_oxidase,_copper/topa_quinone-
containing_mrna,_complete_cds
u12140_3433-3673,tyrosine_kinase_receptor_p145trk-b_(trk-b)_mrna,_complete_cds_
- 10 u23850_8177-8697,inositol_1,4,5_trisphosphate_receptor_typemrna,_partial_cds
u24488_2519-3042,tenascin-x_(xa)_mrna,_complete_cds
u25771_1383-1821,adp-ribosylation_factor_mrna,_complete_cds
u52373_1810-2355,serine/threonine_kinase_mnb_(mnb)_mrna,_complete_cds
u57623exon#1-4_51-
- 15 240:in_reversesequence,_6798,fatty_acid_binding_protein_fabp_gene,_complete_cds_
u80034_1785-
2283,mitochondrial_intermediate_peptidase_precursor_(mipep)_mrna,_mitochondrial_gene_enc
u81599_751-1273,homeodomain_protein_hoxb13_mrna,_complete_cds
u86214_1736-2000,fas-associated_death_domain_protein_interleukin-1b-
converting_enzymemrna,_complete_
- 20 u88898_561-757,endogenous_retroviral_h_protease/integrase-
derived_orf1_mrna,_complete_cds,_and_putat
all_x07618_880-1388,mrna_for_cytochrome_p450_db1_variant_a_
all_x07730_1535-1680,mrna_for_prostate_specific_antigen
- 25 all_x14253_1410-2003,mrna_for_cripto_protein_
all_x66867_1864-2066:in_x66867cds#2_310,_max_gene_extracted_frommax_gene_
x94628mrna_952-1510,mecp-2_gene_
x99688_3790-4270,mrna_from_tyl_gene
all_y08613_599-1164,alternative_3'_utr_of_nup88_mrna/gb=y08613_/ntype=rna
- 30 z35227cds_385-547:in_reversesequence,_1162-1318,ttf_mrna_for_small_g_protein
- Metagene 98
- ab002559_1302-1746,mrna_for_hunc18b2,_complete_cds_
35 af006087_237-777,arp2/3_protein_complex_subunit_p20-
arc_(arc20)_mrna,_complete_cds/gb=af006087_/ntyp
d10511cds_860-1256:in_reversesequence,_165-243,gene_for_mitochondrial_acetoacetyl-
coa_thiolase
d26308_241-691,mrna_for_nadph-flavin_reductase,_complete_cds_

- d26598_187-571,mrna_for_proteasome_subunit_hsc10-ii,_complete_cds
d31764_1478-1982,mrna_for_kiaa0064_gene,_complete_cds
d38047_327-825,mrna_for_26s_proteasome_subunit_p31,_complete_cds_
d38751_1539-1868:not_in_gb_record,mrna_for_kid_(kinesin-
5 like_dna_binding_protein),_complete_cds_
d43947_6379-6901,mrna_for_kiaa0100_gene,_complete_cds
d50645_502-1006,mrna_for_sdf2,_complete_cds
d85433_109-439,murr1_mrna,_sequence/gb=d85433_/ntype=rna_
hg3638-ht3849_s_at_hg3638-ht3849_amyloid_beta_(a4)_precursor_protein,_altsplice_2,_a4(751)_
10 j04444cds_596-944:in_reversesequence,_3590-3740,cytochrome_c-1_gene,_complete_cds_
l20320cds_605-
953:in_reversesequence,_1218,protein_serine/threonine_kinase_stk1_mrna,_complete_cds
l37042mrna_960-1314,casein_kinase_i_alpha_isoform_(csnk1a1)_mrna,_complete_cds
l40410mrna_296-803,thyroid_receptor_interactor_(trip3)_mrna,_3'_end_of_cds
15 l41559mrna_61-475,pterin-4a-carbinolamine_dehydratase_(pcbd)_mrna,_complete_cds_
m15661mrna_3-338,ribosomal_protein_mrna,_complete_cds
m19483cds_1127-1559:in_reversesequence,_2162-2204,atp_synthase_beta_subunit_gene
m29971_282-750,6-o-methylguanine-dna_methyltransferase_(mgmt)_mrna,_complete_cds_
m55153_2794-3232,transglutaminase_(tgase)_mrna,_complete_cds_
20 u34343_110-560,13kd_differentiation-associated_protein_mrna,_partial_cds/gb=u34343_/ntype=rna
u43923_888-1410,transcription_factor_supt4h_mrna,_complete_cds_
u65093_466-838,msg1-related_gene(mrg1)_mrna,_complete_cds_
u79262_878-1007,deoxyhypusine_synthase_mrna,_complete_cds
u79718_532-1012,endonuclease_iii_homolog(octs3)_mrna,_complete_cds
25 all_x90857_2739-3184,mrna_for_-14_gene,_containing_globin_regulatory_element_
x94910_333-861:not_in_gb_record,mrna_for_erp31_protein
y08766cds_1803-1893:in_reversesequence,_2190-2239,mrna_for_splicing_factor,_sfl-bo_isoform
y12478_210-750,mrna_for_chd5_protein_
30 Metagene 464

d16593_290-812,bdr-2_mrna_for_hippocalcin,_complete_cds
d88460_1233-1695,mrna_for_n-wasp,_complete_cds_
d89016_1618-2116,mrna_for_neuroblastoma,_complete_cds
35 hg2280-ht2376_at_hg2280-ht2376_d-amino-acid_oxidase
hg908-ht908_at_hg908-ht908_mg61_protein
l00635_1029-1437,farnesyl-protein_transferase_beta-subunit_mrna,_complete_cds
l34355_827-961,(clone_p4)_50_kd_dystrophin-associated_glycoprotein_mrna,_complete_cds_
l36818_4098-4608,(clone_51c-3)_51c_protein_mrna,_complete_cds

- 144140exon#61-62_44-
 221:not_in_gb_record_dnl1l_gene_extracted_fromchromosome_x_region_from_filamin_
 m38258_2000-2486,retinoic_acid_receptor_gammamma_complete_cds_
 m77348mrna_1757-1786,pmelmrna_complete_cds_
5 m92432_3098-3566,retinal_guanylyl_cyclase_(retgc)_mrna_complete_cds
 m96759mrna_783-1299,rod_outer_segment_membrane_protein(rom1)_gene_exons_1-
 3_complete_cds
 all_s58733_264-
 357_pp52=b_lymphocyte_signal_transduction_gene_{group_3_inverted_repeat}[human_tu
10 u07418_2004-2454,dna_mismatch_repair_(hmlh1)_mrna_complete_cds
 u37529_556-1030,substance_p_beta-ppt-a_mrna_complete_cds
 u43177exon#1_62-464,urocortin_gene_complete_cds_
 u49928_2513-3035,tak1_binding_protein(tab1)_mrna_complete_cds
 u62966_2137-2635,na+/nucleoside_cotransporter_(hcnt1a)_mrna_complete_cds
15 u68536_1918-2410,zinc_finger_protein_mrna_complete_cds
 u71087_1092-1126,map_kinase_kinase_mek5b_mrna_complete_cds
 u92314_840-1415,hydroxysteroid_sulfotransferase_sult2b1a_(hsst2)_mrna_complete_cds.
 all_x06256_3681-4180,mrna_for_fibronectin_receptor_alpha_subunit_
 all_x13589_2395-2936,mrna_for_aromatase_(estrogen_synthetase)
20 all_x54871_1059-1612,mrna_for_ras-related_protein_rab5b
 all_x86681_1848-2257,mrna_for_nucleolar_protein_hnp36_
 all_x94453_2396-2907,mrna_for_pyrroline_5-carboxylate_synthetase_

 Metagene 360
25
 d28137_395-743,mrna_for_bst-2_complete_cds
 j04164_366-804,interferon-inducible_protein_27-sep_mrna_complete_cds
 l22342_672-810,nuclear_phosphoprotein_mrna_complete_cds_
 m13755mrna_33-591,interferon-induced_17-kda/15-kda_protein_mrna_complete_cds
30 m31724mrna_2694-3168,phosphotyrosyl-protein_phosphatase_(ptp-1b)_mrna_complete_cds
 m62505_1952-2240,c5a_anaphylatoxin_receptor_mrna_complete_cds_
 u12255_905-1391,igg_fc_receptor_hfern_mrna_complete_cds_
 u50648mrna_2211-2751,interferon-inducible_rna-dependent_protein_kinase_(pkr)_gene
 u72882_448-1009,interferon-induced_leucine_zipper_protein_(ifp35)_mrna_partial_cds
35 u95006_114-654,d9_splice_variant_a_mrna_complete_cds
 x00371mrna_495-1011,myoglobin_gene_(exon_1)_and_joined_cds)
 all_x02874_1063-1298,mrna_for_(2'-5')_oligo_a_synthetase_e_(1,6_kb_ma)
 all_x02875_158-628,mrna_(3'-fragment)_for_(2'-5')_oligo_a_synthetase_e_(1,8_kb_ma)_

all_x57351_294-891,1-8d_gene_from_interferon-inducible_gene_family,1-
 8d_gene_from_interferon-inducib
 x79882cds_2116-2656:in_reversesequence,_2773,lrp_mrna_
 x85116_rnal_s_at_x85116_x85116,not_in_gb_record,epb72_gene_exon_1_

5

Metagene 335

k02882cds_660-1098,_ighd_gene_(immunoglobulin_delta-
 chain)_extracted_fromgermline_igd_chain_gene,_c-
 10 m61199_1227-1689,cleavage_signalprotein_mrna,_complete_cds

Metagene 328

- d25274_727-1177,randomly_sequenced_mrna
- 15 d49396_948-1446,mrna_for_apo1(mer5(aop1-mouse)-like_protein),_complete_cds
 104731_13654-14152,translocation_t(4:11)_of_all-1_gene_to_chromosome_4
 125081_595-1015,gtpase_(rhoc)_mrna,_complete_cds_
 m22538_286-778,nuclear-encoded_mitochondrial_nadh-
 ubiquinone_reductase_24kd_subunit_mrna,_complete_c
- 20 m31951exon#2_671-1061:in_reversesequence,_6169,perforin_(prf1)_gene,_complete_cds_
 m63138mrna_1545-2007,cathepsin_d_(catd)_gene_
 s65738_1061-1373,_actin_depolymerizing_factor_[human,_fetal_brain,_mrna,_1452_nt]_
 u09848_2904-3474,zinc_finger_protein_(znf139)_mrna,_partial_cds
 u43901mrna#1_429-
- 25 557,37_kd_laminin_receptor_precursor/p40_ribosome_associated_protein_gene,_complete
 u83908cds_941-1295:in_reversesequence,_1589-1649,nuclear_antigen_h731_mrna,_complete_cds
 u90878_693-1179,lim_domain_protein_clp-36_mrna,_complete_cds.
 u90902_939-1407,clone_23612_mrna_sequence
 u94855_696-1176,translation_initiation_factor47_kda_subunit_mrna,_complete_cds
- 30 all_x16416_4998-5497,c-abl_mrna_encoding_p150_protein
 all_x51466_2702-3057,mrna_for_elongation_factor_2
 x70218_771-1203,_hsapiens_mrna_for_protein_phosphatase_x
 all_x74929_1365-1706,krt8_mrna_for_keratin_8_
 all_x76228_677-1242,mrna_for_vacuolar_h+_atpase_e_subunit
- 35 x78136cds_688-1060:in_reversesequence,_1130-1244,hnrnp-e2_mrna
 x82207cds_876-1098:in_reversesequence,_1166-1412,mrna_for_beta-centractin_(pc3)
 y08999cds_583-1045:in_reversesequence,_1132,mrna_for_sop2p-like_protein_
 all_z14000_958-1463,ring1_gene_
 all_z49835_1354-1805,mrna_for_protein_disulfide_isomerase

Metagene 213

- hg4321-ht4591_at_hg4321-ht4591_ahnak-related_sequence
- 5 j04449_2290-2776,(clone_nf_10)_cytochrome_p-450_nifedipine_oxidase_mrna,_complete_cds_
j05459mrna_695-1187,glutathione_transferase_m3_(gstm3)_mrna,_complete_cds
117325_73-451,pre-t/nk_cell_associated_protein_(1d12a2)_mrna,_complete_cds_
132164_630-1158,zinc_finger_protein_mrna,_3'_end
m16714exon#8_627-747,mhc_i_divergent_lymphocyte_antigen_gene,_complete_cds,_clone_rs5
- 10 all_m37457_334-371,na+,k+_#name?_catalytic_subunit_alpha-
iii_isoform_gene,na+,k+_#name?_catalytic_su
all_m86808_2578-2977,pyruvate_dehydrogenase_complex_(pdha2)_gene,_complete_cds_
all_x58723_1862-2049,mdr1_(multidrug_resistance)_gene_for_p-glycoprotein_
x92368mrna_5695-6187,ncx1_gene_(exon_1)/gb=x92368_/ntype=dna_/annot=mrna_

15

Metagene 92

- d14826_834-1163,mrna_for_hcrem_(cyclic_amp-responsive_element_modulator)_typeprotein,_complete_cds
- 20 hg2591-ht2687_s_at_hg2591-ht2687_transcription_factor_itf-1
u13696cds_2138-2563:in_reversesequence,_2600-
2669,homolog_of_yeast_mutl_(hpm2)_gene,_complete_cds
u60269cds#3_237-447:in_reversesequence,_1593-1737,endogenous_retrovirus_herv-
k(hml6)_proviral_clone_
25 x84740mrna_2847-3309,mrna_for_dna_ligase_iii_
y10275cds_363-633:in_reversesequence,_880-1060,mrna_for_l-3-phosphoserine_phosphatase_

Metagene 64

- 30 hg2702-ht2798_r_at_hg2702-ht2798_serine/threonine_kinase_
s79781mrna_31-
169,_wt1_{antisense_promoter,_intron_1}[human,kidney_genomic,_780_nt]/gb=s79781_/nt
x54162mrna_3362-3818,mrna_for_a_64_kd_autoantigen_expressed_in_thyroid_and_extra-
ocular_muscle_
35 x61118mrna_1457-1955,_ttg-2a_gene_extracted_fromttg-
2_mrna_for_a_cysteine_rich_protein_with_lim_moti
y13896_4-179,skeletal_muscle_alternate_5'_end_of_gene_kir4.2_5'_utr/gb=y13896_/ntype=rna

Metagene 45

- d38163_3117-3661,mrna_for_al(xix)_collagen_chain,_complete_cds_
 all_x03066_787-1268,mrna_for_hla-d_ii_antigen_do_beta_chain
 x14766mrna_1363-1711,mrna_for_gaba-a_receptor,_alphasubunit_
5 x76104cds_4113-4257:in_reversesequence,_4629-4827,dap-kinase_mrna_
 z34974cds_1816-2144:in_reversesequence,_2439-2515,mrna_for_plakophilin_(partial)

Metagene 447

- 10** af006084_935-1277,arp2/3_protein_complex_subunit_p41-
 arc_(arc41)_mrna,_complete_cds/gb=af006084_/nty
 d00017_851-1319,lipocortin_ii_mrna_
 d26129_1145-1577,mrna_for_ribonuclease_a_(rnase_a),_complete_cds_
 d42043_2329-2863,mrna_for_kiaa0084_gene,_partial_cds_
15 d87292_572-1052,mrna_for_rhodanese,_complete_cds_
 d88152_2081-2639,mrna_for_acetyl-coenzyme_a_transporter,_complete_cds
 j04456_31-469,_humankd_lectin_mrna,_complete_cds
 l13720_1860-2436,growth-arrest-specific_protein_(gas)_mrna,_complete_cds
 l25080_1212-1692,gtp-binding_protein_(rhoa)_mrna,_complete_cds_
20 l33075_6978-7530,ras_gtpase-activating-like_protein_(iqgap1)_mrna,_complete_cds_
 l40379mrna_181-541,thyroid_receptor_interactor_(trip10)_mrna,_3'_end_of_cds_
 l41147mrna_1383-1959,5-ht6_serotonin_receptor_mrna,_complete_cds
 m13450_636-1020,esterase_d_mrna,_3'_end
 all_m14338_2740-3281,mrna_for_protein_s_and_intron_
25 all_m14949_1905-2423,r-ras_gene
 m23294mrna#1_1219-1651,beta-hexosaminidase_beta-subunit_(hexb)_gene
 m26576exon_43-289:not_in_gb_record,col4a1_gene_(alpha-
 l_type_iv_collagen)_extracted_fromalpha-1_col
 m27492_4336-4864,interleukinreceptor_mrna,_complete_cds_
30 m28713exon_536-1052,nadh-cytochrome_b5_reductase_(b5r)_gene_
 m33680_879-1431,26-kda_cell_surface_protein_tapa-1_mrna,_complete_cds
 m36341_912-1458,adp-ribosylation_factor(arf4)_mrna,_complete_cds
 m63256_1975-2497,major_yo_paraneoplastic_antigen_(cdr2)_mrna,_3'_end_
 m64571mrna_4553-4931,microtubule-associated_proteinmrna,_complete_cds_
35 m76378mrna_1294-1768,cysteine-rich_protein_(crp)_gene
 m82809_1465-1915,annexin_iv_(anx4)_mrna,_complete_cds
 m83751_539-1013,arginine-rich_protein_(arp)_gene,_complete_cds_
 u01691mrna_1257-1743,annexin_v_(anx5)_gene,_5'_-untranslated_region
 u02570_2792-3290,cdc42_gtpase-activating_protein_mrna,_partial_cds_

- u44378_2091-
 2655,homozygous_deletion_target_in_pancreatic_carcinoma_(dpc4)_mrna,_complete_cds
 u46006_140-620,smooth_muscle_lim_protein_(h-
 smlim)_mrna,_complete_cds/gb=u46006_/ntype=rna_
- 5 u46499_at_u46499_u46499,not_in_gb_record,microsomal_glutathione_transferase_(gstl2)_gene,_5'
 _sequenc
 u93205_588-1020,nuclear_chloride_ion_channel_protein_(ncc27)_mrna,_complete_cds
 x04412cds_2047-2305:in_reversesequence,_2421-2529,mrna_for_plasma_gelsolin
 all_x05610_1701-2098,mrna_for_type_iv_collagen_alpha_-2_chain
- 10 all_x07979_3223-3596,mrna_for_fibronectin_receptor_beta_subunit
 all_x54304_391-878,mrna_for_myosin_regulatory_light_chain
 y00433cds_233-581:in_reversesequence,_905-
 1109,mrna_for_glutathione_peroxidase_(ec_1.11.1.9.)_
- 15 Metagene 70

 u02687_2874-3312,growth_factor_receptor_tyrosine_kinase_(stk-1)_mrna,_complete_cds_
 u79271_596-1130,clones_23920_and_23921_mrna_sequence_
- 20 Metagene 191

 hg3415-ht3598_at_hg3415-ht3598_poliovirus_receptor_
 j00124exon#8_14-227:not_in_gb_record,50_kda_type_i_epidermal_keratin_gene,_complete_cds
 all_100205_358-503,k6b_(epidermal_keratin,_type_ii)_gene_
- 25 l35594mrna_3002-3178,autotaxin_mrna,_complete_cds
 l42611_1374-1954,keratinisoform_k6e_(krt6e)_mrna,_complete_cds_
 m14676_1864-2332,src-like_kinase_(slk)_mrna,_complete_cds
 m95585mrna_3253-3805,hepatic_leukemia_factor_(hlf)_mrna,_complete_cds
 u41518_1761-2253,channel-like_integral_membrane_protein_(aqp-1)_mrna,_clone_aqp-1-
 2344,_partial_cds
- 30 u77180_55-511,macrophage_inflammatory_proteinbeta_(mip-3beta)_mrna,_complete_cds
 all_x06182_4474-5069,c-kit_proto-oncogene_mrna_
 x61123mrna_1212-1608,btg1_mrna_
- 35 Metagene 27

 ac002073cds#1_507-759:in_reversesequence,_23812-
 24010,_wugsc:dj515n1.2_gene_extracted_frompac_clone_
 hg3345-ht3522_at_hg3345-ht3522_pou_domain-containing_protein_

- l37036exon#2_29-92:in_reversesequence, 1754-1971, neutrophil-activating peptide_78_(ena-78)_gene, _com
- m15169mrna#1_1704-1950:in_reversesequence, 3390-3408, beta-2-adrenergic_receptor_mrna, _complete_cds
- 5** m25756_1777-2287, secretogranin_ii_gene, _complete_cds_
m28983_1823-2369, interleukin alpha_(il_1)_mrna, _complete_cds_
m33317mrna_1158-1693, cytochrome_p450iia4_(cyp2a4)_mrna, _complete_cds_
m62486exon_17-359:not_in_gb_record, c4b-binding_protein_gene_
u66580cds_510-1026:in_reversesequence, 1075-1081, putative_g_protein-
10 coupled_receptor_(gpr21)_gene, _c
u79242_1043-1589, clone_23560_mrna_sequence_
all_x02404_227-
750, mrna_fragment_for_second_calcitonin_gene_related_peptide_(cgrp)_from_medullary_th
x55005mrna_2002-2230, c-erba-1_mrna_for_thyroid_hormone_receptor_alpha_
15 x77533cds_982-1390:in_reversesequence, 1532-1544, mrna_for_activin_type_ii_receptor
all_z11933_1730-1942, mrna_for_n-oct_3, _n-oct5a, _and_n-oct_5b_proteins
- Metagene 444
- 20** af014958_1175-1619, chemokine_receptor_x_(ckrx)_mrna, _complete_cds/gb=af014958/_ntype=rna
d16688_876-1448, ltg9/mlt3_mrna, _c-terminal
d29956_3758-4328, mrna_for_kiaa0055_gene, _complete_cds
d31888_4700-5186, mrna_for_kiaa0071_gene, _partial_cds_
d38037_292-826, mrna_for_fk506-binding_protein_12kda_(hfkbp-12)_homologue, _complete_cds_
25 d63135mrna_31-499, mrna_for_ets-like_30_kda_protein/gb=d63135/_ntype=rna
d79987_6109-6523, mrna_for_kiaa0165_gene, _complete_cds
d86957_3869-4265, mrna_for_kiaa0202_gene, _partial_cds_
d88213_2085-2481, mrna_for_retina-specific_amine_oxidase, _complete_cds
hg2383-ht4824_s_at_hg2383-ht4824_cystathionine_beta_synthase, _altsplice_3
30 hg25930-ht26386_at_hg25930-ht26386_estradiol_17-beta_dehydrogenase
hg2841-ht2968_s_at_hg2841-ht2968_albumin, _altsplice_1
hg2987-ht3136_s_at_hg2987-ht3136_vasoactive_intestinal_peptide_
hg3264-ht3441_at_hg3264-ht3441_af-6
hg4027-ht4297_f_at_hg4027-ht4297_beta-1-glycoprotein, _domains_n_and_ii_, _pregnancy-specific
35 hg4390-ht4660_at_hg4390-ht4660_ribosomal_protein_118a_homolog
l06133_7979-8435, putative_cu++-transporting_p-type_atpase_mrna, _complete_cds_
all_l08904_1372-1667, h2k_binding_factor(kbf2)_mrna, _complete_cds_
l12468_3246-3780, aminopeptidase_a_mrna, _complete_cds
l14812_3349-3936, retinoblastoma_related_protein_(p107)_mrna, _complete_cds

- 120826_3074-3572,i-plastin_mrna,_complete_cds
 122569_1685-2243,cathepsin_b_mrna,_3' utr_with_a_stem-
 loop_structure_providing_mrna_stability_
 139060mrna_1037-1547,transcription_factor_sl1_mrna,_complete_cds
- 5** m11025mrna_783-1263,asialoglycoprotein_receptor_h2_mrna,_complete_cds
 m17252mrna_934-1198,cytochrome_p450c21_mrna,_3' end
 all_m24364_1059-
 1435,mhc_ii_lymphocyte_antigen_dqb_mrna,_complete_cds,_haplotype_dr7,_dqw9_
 m29581_1469-1853,zinc-finger_protein(zfp8)_mrna,_3' end
- 10** m57464_3899-4439,ret_proto-oncogene_mrna,_complete_cds_
 m63962mrna_2985-3507,gastric_h,k-atpase_catalytic_subunit_gene,_complete_cds
 m74525_2002-2536,hhr6b_(yeast_radhomologue)_mrna,_complete_cds
 m87860cds_25-331:in_reversesequence,_176-212,s-lac_lectin_1-14-ii_(lgals2)_gene_
 m89955cds_635-1085:in_reversesequence,_1391-1439,5-ht1d-
 type_serotonin_receptor_gene,_complete_cds
- 15** s48983cds_36-282:in_reversesequence,_204-
 408,_saa4=serum_amyloid_a_[human,_genomic,_858_ntsegments]
 s59184_2487-2979,_ryk=related_to_receptor_tyrosine_kinase_[human,_hepatoma,_mrna,_3068_nt]
 s61953_516-798,_c-
- 20** erbb3=receptor_tyrosine_kinase_{alternatively_spliced}_[human,_gastric_cancer_cell
 u16811_1491-2034,bak_mrna,_complete_cds
 all_u18914_2694-3199,19.8_kda_protein_mrna,_complete_cds_
 u28758_45-626,nmda_receptor_subtype_2b_subunit_(grin2b)_mrna,_partial_cds
 u40215_1479-2049,synapsin_iib_mrna,_complete_cds_
- 25** u40763_2251-2803,clk-associated_rs_cyclophilin_cars-cyp_mrna,_complete_cds_
 u43286_1633-2155,selenophosphate_synthetase(sps2)_mrna,_complete_cds
 u44848_7-187,nuclear_respiratory_factor(nrfl)_mrna,_3' utr/gb=u44848_/ntype=rna_
 u48807_1652-2156,map_kinase_phosphatase_(mkp-2)_mrna,_complete_cds_
 u49974cds_444-
- 30** 1017,mariner2_transposable_element,_complete_consensus_sequence/gb=u49974_/ntype=dna/
 u52518_399-825,grb2-related_adaptor_protein_(grap)_mrna,_complete_cds
 u71092cds_954-1158:in_reversesequence,_1611-1767,somatostatin_receptor-
 like_protein_(slc1)_gene,_com
 u79257_952-1432,clone_23932_mrna_sequence
- 35** u88666_3113-3653,serine_kinase_srp_k2_mrna,_complete_cds
 all_u90552_3170-
 3242,butyrophilin_(btf5)_mrna,_complete_cds,butyrophilin_(btf5)_mrna,_complete_cds
 u90912_1074-1584,clone_23865_mrna_sequence_
 u94332_761-1331,osteoprotegerin_(opg)_mrna,_complete_cds.

- all_x06268_1159-1337,mrna_for_pro-alpha(ii)_collagen_3'_end_c-termtriple_helical_and_c-terminal_non-
- all_x13956_694-1163,12s_rna_induced_by_poly(ri),_poly(rc)_and_newcastle_disease_virus
- x15954mrna_729-1240,mbp1_gene_exon(and_joined_cds)
- 5** x16707cds_379-733:in_reversesequence,_869-923,fra-1_mrna
- x17360mrna_4536-5034,hox_5.1_gene_for_hox_5.1_protein_
- all_x63575_3903-4466,mrna_for_plasma_membrane_calcium_atpase_
- all_x64838_5256-5833,mrna_for_restin_
- x66171cds_341-623:in_reversesequence,_892-1108,cmrf35_mrna,_complete_cds
- 10** all_x77383_1094-1599,mrna_for_cathepsin-o
- x78031_1113-1629,alpha-1,_3-fucosyltransferase_mrna
- all_x95289_48-625,mrna_for_hcgix_protein_
- y11651cds_750-960:in_reversesequence,_1250-1466,mrna_for_phosphate_cyclase
- 15** Metagene 369
- d86966_4491-5031,mrna_for_kiaa0211_gene,_complete_cds
- d87074_6650-7184,mrna_for_kiaa0237_gene,_complete_cds
- hg1862-ht1897_at_hg1862-ht1897_calmodulin_type_i_
- 20** hg825-ht825_at_hg825-ht825_guanine_nucleotide-binding_protein,_alpha_12
- l08424_1124-1586,achaete_scute_homologous_protein_(ash1)_mrna,_complete_cds_
- l23116_3296-3644,galactocerebrosidase_(galc)_mrna,_complete_cds_
- m34715mrna_1750-2206,pregnancy-specific_beta-1-glycoprotein_mrna_psg95,_complete_cds_
- m57423_485-1016,phosphoribosylpyrophosphate_synthetase_subunit.iii_mrna,_3'_end.
- 25** m80359_2409-2835,protein_p78_mrna,_complete_cds
- s69370_234-
- 761,_pax3b=transcription_factor_{alternatively_spliced}_[human,_adult_cerebellum,_mrna,_8
- u25750_3002-3380,chromosome_17q21_mrna_clone_1046:1-1
- u35139_1111-1507,neclin_related_protein_mrna,_complete_cds_
- 30** u39447_3452-3980,placenta_copper_monamine_oxidase_mrna,_complete_cds_
- u42390_8359-8863,trio_mrna,_complete_cds
- u82130_1151-1451,tumor_susceptibility_protein_(tsg101)_mrna,_complete_cds_
- x53793cds_873-
- l227,ade2hl_mrna_showing_homologies_to_saicar_synthetase_and_air_carboxylase_of_the_pu
- 35** x54150mrna_978-1530,mrna_for_fc_receptor_
- x63422cds_305-461:in_reversesequence,_688-916,mrna_for_delta-
- subunit_of_mitochondrial_f1f0_atp-synth
- all_x63546_7261-7856,mrna_for_tre_oncogene_(clone_210)_
- all_z25535_4922-5463,mrna_for_nuclear_pore_complex_protein_hnup153_

Metagene 441

- d16350_1280-1826,sa_mrna_for_sa_gene_product,_complete_cds_
5 d38073_2590-3022,mrna_for_hrlf_beta_subunit_(p102_protein),_complete_cds_
d63481_4350-4890,mrna_for_kiaa0147_gene,_partial_cds_
142373mrna_2651-3071,protein_phosphatase_2a_b56-alpha_mrna,_complete_cds
m29277_2335-
2901,isolate_juso_muc18_glycoprotein_mrna_(3'_variant),_complete_cds,isolate_juso_muc18_
10 m34458mrna_1900-2463,lamin_b_mrna,_complete_cds_
u33286_2642-3092,chromosome_segregation_gene_homolog_cas_mrna,_complete_cds
u37426_4269-4815,kinesin-like_spindle_protein_hksp_(hksp)_mrna,_complete_cds_
u53204_14286-14721,plectin_(plec1)_mrna,_complete_cds
u56816_1376-1838,kinase_myt1_(myt1)_mrna,_complete_cds.
15 u73843_1356-1860,epithelial-specific_transcription_factor_ese-1b_(ese-1)_mrna,_complete_cds
all_x74331_1801-2288,mrna_for_dna_primase_(subunit_p58)
all_x99459_1516-1799,mrna_for_sigma_3b_protein_
y00486mrna_252-
786,_adenine_phosphoribosyltransferase_(aprt)_gene_extracted_fromaprt_gene_for_adenin
20 all_z22555_2041-2516,encoding_cla-1_mrna_
z37986cds_409-631:in_reversesequence,_826-1000,mrna_for_phenylalkylamine_binding_protein

Metagene 407

- 25** d28539_4017-4549,mrna_for_metabotropic_glutamate_receptor_subtype_5b,_complete_cds_
d83195cds_448-802:in_reversesequence,_3957-
3963,dnase1_gene_for_deoxyribonuclease_i,_complete_cds_
m21665mrna_1535-1621,beta-myosin_heavy_chain_mrna,_3'_end
m32315_3202-3604,tumor_necrosis_factor_receptor_mrna,_complete_cds_
30 z70295exon#2-3_7-252:not_in_gb_record,gcap-ii_gene

Metagene 390

- d88795_13-379,mrna_for_cadherin,_partial_cds/gb=d88795/_ntype=rna_
35 d88797_49-379,mrna_for_cadherin,_partial_cds/gb=d88797/_ntype=rna_
hg273-ht273_s_at_hg273-ht273_lymphocyte_antigen_hla-g3_
hg3454-ht3647_at_hg3454-ht3647_zinc_finger_protein_
hg644-ht644_at_hg644-ht644_histone_h1.1
135251mrna_801-1281,extracellular_matrix_protein_(mfap3)_gene,_complete_cds

- all_m11437_1562-
 2440,_kng_gene_(kininogen)_extracted_fromkininogen_gene,_kng_gene_(kininogen)_extrac
 u28727_7835-8357,pregnancy-associated_plasma_protein-
 a_preproform_(pappa)_mrna,_complete_cds_
5 u43279_3409-3955,nucleoporin_nup_36_mrna,_complete_cds/gb=u43279_/ntype=rna
 x05615cds_7824-8238:in_reversesequence,_8327-8423,mrna_for_thyroglobulin
 x51823cds_5-34,mrna_for_b-
 subunit_of_coagulation_factor_xiii_(fxiiib)_(partial)/gb=x51823_/ntype=rna
 x82279exon_54-169,fas,_apo-
10 1_gene_(promoter_and_exon_i)/gb=x82279_/ntype=dna_/annot=exon_
 Metagene 254
- d28118_1807-2263,mrna_for_db1,_complete_cds
15 d45370mrna_13-
 337,apm2_mrna_for_gs2374_(unknown_product_specific_to_adipose_tissue),_complete_cds
 hg2465-ht4871_at_hg2465-ht4871_dna-binding_protein_ap-2,_altsplice_3_
 m31682mrna_2130-2526,testicular_inhibin_beta-b-subunit_mrna,_3'_end
 m86933_220-
20 681,amelogenin_(amely)_mrna,_complete_cds,amelogenin_(amely)_mrna,_complete_cds
 u28249_919-1405,11kd_protein_mrna,_complete_cds
 u68031_91-301,g_protein-
 coupled_receptor_(strl22)_mrna,_alternatively_spliced_5'_utr_sequence/gb=u68
 x76732cds_975-1221:in_reversesequence,_1464-
25 1518:not_in_gb_record,nefa_protein_mrna,_complete_cds_(d
 Metagene 399
- d87328_5900-6404,mrna_for_hcs,_complete_cds
30 j05096mrna_5006-5456,na,k-atpase_subunit_alpha(atp1a2)_gene,_complete_cds
 reverse_l76568_31050-
 31356,_s26_fromexcision_and_cross_link_repair_protein_(ercc4)_gene,_complete_ge
 all_u67092_1093-1868:not_in_gb_record,ataxia-
 telangiectasia_locus_protein_(atm)_gene,_exons_1a,_1b,_
35 all_x13227_1080-1567,mrna_for_d-amino_acid_oxidase_(ec_1.4.3.3)
 x59710cds_75-585:in_reversesequence,_714,mrna_for_caat-
 box_dna_binding_protein_subunit_b_(nf-yb)
 x64559cds_202-580:in_reversesequence,_679-823,mrna_for_tetranectin

Metagene 275

- j04168_1867-2263,leukosialin_mrna_complete_cds
 105515_2108-2594,camp_response_element-binding_protein_(cre-bp1)_mrna_complete_cds_
5 109190mrna_6480-6930,trichohyalin_(trhy)_gene_complete_cds_
 m26602_181-469,defensinprotein_mrna_complete_cds_
 u79245_1139-1541,clone_23586_mrna_sequence_
 u82668mrna#2_1298-
 1820,_shox_gene_(shoxb)_extracted_fromshox_gene_alternatively_spliced_products_c
10 z18954exon#1-4_126-240:in_reversesequence_246-264,mrna_for_s100d_calcium_binding_protein_

Metagene 268

- d63483_2777-3304,mrna_for_kiaa0149_gene_complete_cds
15 104510_2769-3285,nucleotide_binding_protein_mrna_complete_cds_
 m25322mrna_2577-3039,granule_membrane_protein-140_mrna_complete_cds_
 s76978_29-224,_prostate-
 specific_membrane_antigen_{alternatively_spliced}_[human_primary_prostatic_
 u33429_2481-2994,k+_channel_betasubunit_mrna_complete_cds
20

Metagene 250

- d00760_277-781,mrna_for_proteasome_subunit_hc3_
 d14710_1298-1808,mrna_for_atp_synthase_alpha_subunit_complete_cds_
25 d15057_162-576,mrna_for_dad-1_complete_cds
 d78151_2321-2825,mrna_for_26s_proteasome_subunit_p97_complete_cds_
 d78275_959-1511,mrna_for_proteasome_subunit_p42_complete_cds
 hg1112-ht1112_at_hg1112-ht1112_ras-like_protein_tc4
 hg2855-ht2995_at_hg2855-ht2995_heat_shock_protein_70_kda
30 hg3214-ht3391_at_hg3214-ht3391_metalloprotein_stimulin_
 j02683mrna_629-1066,adp/atp_carrier_protein_mrna_complete_cds_
 j02902mrna_1694-2156,protein_phosphatase_2a_regulatory_subunit_alpha-isotype_(alpha-pr65)_mrna_comp
 j04173_1114-1648,phosphoglycerate_mutase_(pgam-b)_mrna_complete_cds
35 j04973mrna_1023-1485,cytochrome_bc-1_complex_core_protein_ii_mrna_complete_cds
 103532_1898-2372,m4_protein_mrna_complete_cds_
 107633_396-870,(clone_1950.2)_interferon-gamma_ief_ssp_5111_mrna_complete_cds
 126247_131-617,suilisol_mrna_complete_cds
 141351mrna_1269-1695,prostasin_mrna_complete_cds_

- 176159mrna_471-957,frgl_mrna,_complete_cds
 m17733mrna_13-505,thymosin_beta-4_mrna,_complete_cds_
 m38690_584-1106,cd9_antigen_mrna,_complete_cds_
 m55265mrna_1612-2116,casein_kinase_ii_alpha_subunit_mrna,_complete_cds_
5 m57730mrna_975-1437,b61_mrna,_complete_cds_
 m63488_1834-2344,replication_protein_a_70kda_subunit_mrna_complete_cds_
 m93651_1973-2519,set_gene,_complete_cds
 s80343_1609-2077,_args=arganyl-trna_synthetase_[human,_ataxia-telangiectasia_patients,_ebv-lymphobl
10 u03100_2985-3501,alpha2(e)-catenin_mrna,_complete_cds
 u06155cds_43-
 495,chromosome_1q_subtelomeric_sequence_d1s553/gb=u06155_/ntype=dna_/annot=cds,chromoso
 u15008_25-433,snrnp_core_protein_sm_d2_mrna,_complete_cds
 u18919_408-948,chromosome_17q12-21_mrna_clone_pov-2,_partial_cds
15 u25849mrna_1717-2137,red_cell-
 type_low_molecular_weight_acid_phosphatase_(acp1)_gene,_5'_flanking_re
 u30825_528-1014,splicing_factor_srp30c_mrna,_complete_cds
 u32944_162-540,cytoplasmic_dynein_light_chain(hd1c1)_mrna,_complete_cds_
 u38846_1294-1732,stimulator_of_tar_rna_binding_(srb)_mrna,_complete_cds
20 u39317_16-484,e2_ubiquitin_conjugating_enzyme_ubch5b_(ubch5b)_mrna,_complete_cds_
 u51678_276-756,small_acidic_protein_mrna,_complete_cds_
 u52427mrna_239-773,rna_polymerase_ii_seventh_subunit_(rpb-7)_gene,_complete_cds.
 u60276_645-1191,hasna-i_mrna,_complete_cds_
 u73514_376-892,short-chain_alcohol_dehydrogenase_(xh98g2)_mrna,_complete_cds.
25 u73824_3202-3766,p97_mrna,_complete_cds
 u77396_at_u77396_u77396,not_in_gb_record,tnf-
 alpha_inducible_responsive_element_mrna,_complete_cds
 x00351cds_855-1065:in_reversesequence,_1154-1376,mrna_for_beta-actin
 all_x15183_2479-2894,mrna_for_90-kda_heat-shock_protein
30 all_x53331_31-590,mrna_for_matrix_gla_protein
 all_x57206_3916-4487,mrna_for_1d-myo-inositol-trisphosphate_3-kinase_b_isoenzyme_
 x57959cds_264-714,mrna_for_ribosomal_protein_17
 x60036cds_683-1037:in_reversesequence,_1163-
 1223,mrna_for_mitochondrial_phosphate_carrier_protein_
35 x63563cds_3176-3500,mrna_for_rna_polymerase_ii_140_kda_subunit_
 x75091cds_300-653:in_reversesequence,_848-892,mrna_for_hla-dr_associated_protein_ii_(phapii)
 all_x81817_933-1240,bap31_mrna_
 x83218cds_215-539,mrna_for_atp_synthase
 all_x96752_1367-1818,mrna_for_1-3-hydroxyacyl-coa_dehydrogenase

y12711_336-864,mrna_for_putative_progestrone_binding_protein
 z35402mrna_3912-4402,gene_encoding_e-cadherin_exonand_joined_cds
 z50853cds_556-802:in_reversesequence_833-1001,mrna_for_clpp

5 Metagene 67

hg2171-ht2241_at_hg2171-ht2241_12-lipoxygenase_
 m97347_1499-2060,beta-1,6-n-acetylglucosaminyltransferase_mrna_complete_cds_
 u46116mrna_5907-6477,receptor_tyrosine_phosphatase_gamma_(ptprg)_gene
 10 all_u83600_202-
 527,death_domain_receptor(DDR3)_mrna_alternatively_spliced_form_2_partial_cds/gb=u8
 all_x95715_1306-1901,mrna_for_anthracycline_resistance_associated_protein

Metagene 293

15

102320_1463-1997,radixin_mrna_complete_cds
 m86868_1189-1585,gamma_amino_butyric_acid_(GABA_RHO2)_gene_mrna_complete_cds

Metagene 448

20

ab000449_1091-1607,mrna_for_vrk1_complete_cds_
 d14689_6077-6557,mrna_for_kiaa0023_gene_complete_cds
 x55668mrna_550-940,mrna_for_proteinase_3_
 all_x75917_1064-1602,mrna_for_fetal_beta-mhc_binding_factor

25

Metagene 127

l24470_1905-2403,prostanoid_fp_receptor_mrna_complete_cds
 all_m36089_2244-2797,dna-repair_protein_(XRC1)_mrna_complete_cds_
 30 m74161_2469-2991,inositol_polyphosphate_5-phosphatase_(5ptase)_mrna_3'_end
 s57235_1085-
 1664_cd68=110kda_transmembrane_glycoprotein_[human_promonocyte_cell_line_u937_mrna_1
 u48231exon#2_1478-2015,bradykinin_b1_receptor_(bdkrb1)_gene_first_
 x51630mrna_2403-2955:in_reversesequence_2961-
 35 2979,wilms_tumor_wt1_mrna_for_zinc_finger_protein_kru
 x98261cds_121-352:in_reversesequence_388-583,mrna_for_m-phase_phosphoprotein_mpp5_

Metagene 134

- hg4128-ht4398_at_hg4128-ht4398_anion_exchanger_3_cardiac_isoform
j03934_1835-2371_human_nad(p)h:menadione_oxidoreductase_mrna_complete_cds
100634_734-1246_farnesyl-protein_transferase_alpha-subunit_mrna_complete_cds
109717mrna_1316-1778_lyosomal_membrane_glycoprotein-
- 5 2_(lamp2)_gene_5'_end_and_flanking_region
110413_1331-1589_farnesyltransferase_alpha-subunit_mrna_complete_cds
120852_2574-3150_leukemia_virus_receptor(givr2)_mrna_complete_cds
137199_977-1313_(clone_cd24-1)_huntington_disease_candidate_region_mrna_fragment
142025mrna_1988-2504_cellular_co-factor_(rab)_gene_complete_cds_
- 10 m23114mrna_3623-4085_calcium-atpase_(hkl)_mrna_complete_cds
m55150mrna_978-1422_fumarylacetoacetate_hydrolase_mrna_complete_cds_
m91592_1971-2325_zinc-finger_protein_(znf76)_gene_partial_cds_
s82447_42-397_gcn5-
like_1=gcn5_homolog/putative_regulator_of_transcriptional_activation_{clone_gcn5
- 15 u10324_2934-3444_nuclear_factor_nf90_mrna_complete_cds
u24169_723-1197_jtv-1_(jtv-1)_mrna_complete_cds_
u24183_2457-3031_phosphofructokinase_(pfkm)_mrna_complete_cds_
u29091_960-1368_selenium-binding_protein_(hsbp)_mrna_complete_cds/gb=u29091/_ntype=rna
u29463mrna_2121-2681_cytochrome_b561_gene
- 20 u40462_3034-3574_ikaros/lyf-1_homolog_(hik-1)_mrna_complete_cds_
u52153_2069-2513_inwardly_rectifying_potassium_channel_kir3.2_mrna_complete_cds_
u65676_3144-3648_hermansky-pudlak_syndrome_protein_(hps)_mrna_complete_cds
u66669_785-1240:not_in_gb_record_3-hydroxyisobutyryl-
coenzyme_a_hydrolase_mrna_complete_cds
- 25 u68063_1453-1915_transformer-2_beta_(htra-2_beta)_mrna_complete_cds_
u74612_2915-3425_hepatocyte_nuclear_factor-3/fork_head_homolog_11a_(hfh-
11a)_mrna_complete_cds.
u75370_3396-
3732_mitochondrial_rna_polymerase_mrna_nuclear_gene_encoding_mitochondrial_protein_com
- 30 u76272mrna_161-689_diadenosine_triphosphate_(ap3a)_hydrolase_(fhit)_gene_5'_of
u91316_891-1461_acyl-coa_thioester_hydrolase_mrna_complete_cds
all_x06825_679-1154_mrna_for_skeletal_beta-tropomyosin_
x15187cds_2089-2380:in_reversesequence_2521-
2737_tral_mrna_forhomologue_of_murine_tumor_rejection_a
- 35 x61970cds_299-677:in_reversesequence_758-860_mrna_for_macropain_subunit_zeta_
all_x70944_2459-3030_mrna_for_ptb-associated_splicing_factor_
all_x77922_1492-2000_gd3_synthase_mrna_
x85134mrna_2737-3007_rbq-3_mrna_
all_x87176_2148-2593_mrna_for_17-beta-hydroxysteroid_dehydrogenase_

- all_x91788_857-1284,mrna_for_icln_protein
 x95586exon#3_56-248:in_reversesequence,_5872-6088:not_in_gb_record,mb1_gene
 x97795cds_1954-2218:in_reversesequence,_2342-2564,mrna_homologous_to_scerevisiae_rad54
 y08682mrna_2358-2552,mrna_for_carnitine_palmitoyltransferase_i_type_i_
- 5** y11251_4297-4822,mrna_for_novel_member_of_serine-arginine_domain_protein,_srrp129
 z17227_1268-1850,mrna_for_transmembrane_receptor_protein_
 z68129mrna#1_3-469:in_fullsequence,_16183-16321:not_in_gb_record,_h-
 idh_gamma_gene_(nad(h)-specific_
- 10** Metagene 466
- hg3920-ht4521_s_at_hg3920-ht4521_homeotic_protein_a1,_i,_altsplice_1_
 hg4517-ht4920_s_at_hg4517-
 ht4920_immunoglobulin_recombination_signal_sequence_binding_protein,_altsp
- 15** l34155_4838-5306,laminin-related_protein_(lama3)_mrna,_complete_cds_
 m21305cds_39-
 119,alpha_satellite_and_satellitejunction_dna_sequence/gb=m21305/_ntype=dna/_annot=cds_
 u60808_1423-2000,cdp-diacylglycerol_synthase_(cds)_mrna,_complete_cds
 x60673mrna_1091-1649,ak3_mrna_for_adenylate_kinase_3
- 20** Metagene 100
- d28423_53-100,mrna_for_pre-
 mrna_splicing_factor_srp20,_5'_utr_(sequence_from_the_5'_cap_to_the_start
- 25** all_d89377_1587-2173,mrna_for_msx-2,_complete_cds,mrna_for_msx-2,_complete_cds
 l13943_1963-2019,glycerol_kinase_(gk)_mrna_exons_1-4,_complete_cds_
 m37197mrna_2687-3065,ccaat-box-binding_factor_(cbf)_mrna,_complete_cds_
 m68520_1708-2170,cdc2-related_protein_kinase_mrna,_complete_cds
 s67970_962-1538,_znf75=krab_zinc_finger_[human,_lung_fibroblast,_mrna,_1563_nt]_
- 30** s70585mrna_138-612,_thyroid-
 stimulating_hormone_alpha_subunit_[human,_genomic,_1327_ntsegments]_
 s82471_77-298,_ssx3=kruppel-
 associated_box_containing_ssx_gene_[human,_testis,_mrna_partial,_675_nt]
 u04209_1396-1834,associated_microfibrillar_protein_mrna,_complete_cds
- 35** u12978_1713-2247,sperm_membrane_protein_bs-84_(hsd-1)_mrna,_partial_cds
 u15555_1003-1489,serine_palmitoyltransferase_(lcb2)_mrna,_partial_cds
 u18271_cds1_at_u18271_u18271,not_in_gb_record,thymopoietin_(tppo)_gene,thymopoietin_(tppo)
)_gene
 u39226_6864-7440,myosin_viiia_(ush1b)_mrna,_complete_cds

u43843_813-1374,h-neuro-d4_protein_mrna_complete_cds

u82321_1608-2112,clone_14.9b_mrna_sequence_

all_x59618_1970-2475,rr2_mrna_for_small_subunit_ribonucleotide_reductase_

x98482mrna_2-

- 5 46,tnnt2_gene_exon/gb=x98482_/ntype=dna_/annot=mrna,tnnt2_gene_exon/gb=x98482_/ntype=dn

Metagene 59

af001548mrna_6079-

- 10 6385_815a9.1_gene (myosin heavy chain)_extracted_fromchromosomebac_clone_cit987sk

d15049_3317-3845,mrna_for_protein_tyrosine_phosphatase_

l36531mrna_2573-3059,integrin_alphasubunit_mrna_3'_end

l41680_1371-1869,alpha-2,8-polysialyltransferase (pst)_gene_complete_cds_

m17316exon_3-249:in_reversesequence_260-338:not_in_gb_record,gamma-a-

- 15 crystallin_gene (gamma-g5)_

m26061mrna_2449-2890:not_in_gb_record,cgmp_phosphodiesterase_alpha_subunit (cgpr-a)_mrna_complete_c

m73482mrna_757-1279,neuromedin_b_receptor (nmb-r)_mrna_complete_cds_

u43916_147-698,tumor-associated_membrane_protein_homolog (tmp)_mrna_complete_cds

- 20 u46744_2358-2493,dystrobrevin-alpha_mrna_complete_cds_

u94747_838-1276,wd_repeat_protein_han11_mrna_complete_cds/gb=u94747_/ntype=rna

all_x74142_1952-2535,hbf-1_mrna_for_transcription_factor_

y09445cds_1175-1517:in_reversesequence_2206-2368,mrna_for_transcription_factor_tbx5_

- 25 Metagene 87

j05070_1805-2303,type_iv_collagenase_mrna_complete_cds

u22028utr#1_47-

168:in_reversesequence_8031,cytochrome_p450 (cyp2a13)_gene_complete_cds,cytochrome_

- 30 u77968_1294-1879,neuronal_pas1 (npas1)_mrna_complete_cds

x87767exon_4-148,cd89_gene_exon_s1/gb=x87767_/ntype=dna_/annot=exon_

Metagene 195

- 35 d87461_2959-3517,mrna_for_kiaa0271_gene_complete_cds

m26004_3326-3894,cr2/cd21/c3d/epstein-barr_virus_receptor_mrna_complete_cds_

m65254_1710-2184,protein_phosphatase_2a_65_kda_regulatory_subunit-beta_mrna_complete_cds

s81243_2102-

2660_chn=steroid/thyroid_orphan_receptor_homolog_gene [human_fetal_brain_mrna_partial

- u04847_1262-1802,ini1_mrna,_complete_cds_
u18383mrna_2319-2587,nuclear_respiratory_factor(nrf-1)_gene_
u19147_34-66,gage-6_protein_mrna,_complete_cds_
u51920_1447-1927,signal_recognition_particle_(srp54)_mrna,_complete_cds
5 u79290_1380-1770,clone_23908_mrna_sequence_
u97502mrna_2736-3126,butyrophilin_(bt3.3)_gene_
all_x51757_1909-2414,heat-shock_protein_hsp70b'_gene_
x95152mrna_10974-11274,brca2_gene_exon(and_joined_coding_region)_
y10812_767-1253,mrna_for_fructose-bisphosphatase_
10
Metagene 489

m92287_1531-1999,cyclin_d3_(ccnd3)_mrna,_complete_cds_
u32989_1109-1559,tryptophan_oxygenase_(tdo)_mrna,_complete_cds_
15 u90907_1150-1612,clone_23907_mrna_sequence_
all_x99268_928-1367,mrna_for_b-hlh_dna_binding_protein_

Metagene 451

20 d10923_1452-1962,mrna_for_hm74_
d42038_3730-4216,mrna_for_kiaa0087_gene,_complete_cds
d50917_4943-5489,mrna_for_kiaa0127_gene,_complete_cds
d50918_4053-4563,mrna_for_kiaa0128_gene,_partial_cds_
hg2530-ht2626_at_hg2530-ht2626_adenylyl_cyclase-associated_protein
25 hg2796-ht2904_at_hg2796-ht2904_neural_cell_adhesion_molecule_
hg3248-ht3425_at_hg3248-ht3425_fibroblast_growth_factor,_antisense_mrna
all_k01884_587-888,blym-1_transforming_gene,_complete_coding_region
l05568_1937-2459,na+/cl-_dependent_serotonin_transporter_mrna,_complete_cds
l10374_1461-1977,(clone_ctg-a4)_mrna_sequence
30 l11695_1767-2247,activin_receptor-like_kinase_(alk-5)_mrna,_complete_cds_
l13436mrna_3522-4020,guanylate_cyclase_mrna,_complete_mature_peptide
l20321_3112-3655,protein_serine/threonine_kinase_stk2_mrna,_complete_cds_
l22206exon#3_63-639,vasopressin_receptor_v2_gene,_complete_cds_
l38500cds_1574-2102,na+/myo-
35 inositol_cotransporter_(slc5a3)_gene,_complete_cds/gb=l38500/_ntype=dna_
l77563mrna_129-591,dgs-f_partial_mrna/gb=l77563/_ntype=rna
reverse_l78833_2267-
2337,_brca1_gene_extracted_frombrca1_rho7_and_vati_genes,_complete_cds,_and_ipf
m17863mrna_242-822,preproinsulin-like_growth_factor_ii_(igf-ii)_variant_mrna,_complete_cds_

- all_m19720_2034-2557,l-myc_gene_(l-myc_protein)_extracted_froml-myc_protein_gene,_complete_cds,l-m
- m25164cds_5-383:in_reversesequence,_265-1170,thyrotropin_beta_subunit_gene
- m55268mrna_1094-1556,casein_kinase_ii_alpha'_subunit_mrna,_complete_cds
- 5 m62302_1939-2485,growth/differentiation_factor(gdf-1)_mrna,_complete_cds
- m64788_2759-3209,gtpase_activating_protein_(rap1gap)_mrna,_complete_cds
- m65290_1957-2215,natural_killer_cell_stimulatory_factor_(nksf)_mrna,_complete_cds_clone_p40_
- m95549_1774-2194,sodium/glucose_cotransporter-like_protein_mrna,_complete_cds_
- m98776mrna_1864-2266,keratogene,_complete_cds_
- 10 s78432mrna#1_3-87,_un-named-transcript-
- 1_from_sas=transmembraneprotein_{5' region}_[human_sarcomas,
- u10686exon#2_730-1267,mage-11_antigen_(mage11)_gene,_complete_cds
- u12897_1564-1870:in_reversesequence,_1900-1996,non-translated_mrna_sequence_
- u15173_1781-2303,nip2_(nip2)_mrna,_complete_cds
- 15 u23736_779-1348,gata-3_binding_protein_g3b_mrna,_partial_cds.
- u28831_532-964,protein_immuno-reactive_with_anti-ptb_polyclonal_antibodies_mrna,_partial_cds_
- u37352_3505-3961,protein_phosphatase_2a_b'alpha1_regulatory_subunit_mrna,_complete_cds_
- u37431mrna#1_2114-
- 2540,hoxa1_mrna,_long_transcript_and_alternatively_spliced_forms,_complete_cds_
- 20 u43527_180-728:not_in_gb_record,malignant_melanoma_metastasis-suppressor_(kiss-
- l)_gene,_mrna,_comple
- u43944_1705-1978,breast_cancer_cytosolic_nadp(+)-dependent_malic_enzyme_mrna,_partial_cds
- u47931mrna_63-537,g-protein_beta-
- 3_subunit_alternatively_spliced_form_mrna_sequence/gb=u47931_/ntype
- 25 u52830_19-271,cri-du-chat_region_mrna,_clone_csc8.
- u55209_3812-3977,myosin_vii_a_transcriptmrna,_complete_cds_
- u63329cds_1128-1554:in_reversesequence,_1814,muty_homolog_(hmyh)_gene,_complete_cds_
- u84011_6566-
- 7127,glycogen_debranching_enzyme_isoform(agl)_mrna,_alternatively_spliced_isoform,_compl
- 30 x04145cds_286-454:in_reversesequence,_593-689,mrna_for_t-
- cell_receptor_t3_gamma_polypeptide_
- x14690cds_1150-1604:in_reversesequence,_1636-1676,mrna_for_plasma_inter-alpha-
- trypsin_inhibitor_heav
- all_x16983_3252-3787,mrna_for_integrin_alpha-4_subunit_
- 35 all_x65962_1115-1174,mrna_for_cytochrome_p-450_
- all_x79984_16-269,aal_mrna/gb=x79984_/ntype=rna
- x89398exon#7_695-1121,_ung_gene_(uracil-dna-
- glycosylase,_ung2)_extracted_fromung_gene_for_uracil_dna
- all_z48541_4517-5100,mrna_for_protein_tyrosine_phosphatase_

z48579cds_1852-2050:in_reversesequence_2062-2392,mrna_for_disintegrin-
metalloprotease_(partial)_
reverse_z84722_11257-
11453,dna_sequence_from_cosmid_gg4_from_a_contig_from_the_tip_of_the_short_arm_

5

Metagene 252

- d10326_1427-1981,mrna_for_pyruvate_kinase
d49372_197-755,mrna_for_eotaxin_complete_cds
- 10 all_d83407_2601-3184,_zaki-4_mrna_inskin_fibroblast_complete_cds
d87467_5371-5857,mrna_for_kiaa0277_gene_complete_cds
hg167-ht167_s_at_hg167-ht167_hypothetical_protein_npiiy20
hg2810-ht2921_at_hg2810-ht2921_homeotic_protein_pl2
hg3162-ht3339_at_hg3162-ht3339_transcription_factor_iiia
- 15 hg3627-ht3836_at_hg3627-ht3836_calcium_channel_voltage-
gated_betasubunit_1_type_altsplice_2_ske
hg3638-ht3993_s_at_hg3638-ht3993_amyloid_beta_(a4)_precursor_protein_altsplice_4
hg4169-ht4439_s_at_hg4169-ht4439_syntaxin_1b
hg830-ht830_at_hg830-ht830_potassium_channel
- 20 j02645mrna_882-1314,translational_initiation_factor_(eif-2)_alpha_subunit_mrna_complete_cds
k02777_139-621,t-cell_receptor_active_alpha-chain_mrna_from_jurkat_cell_line
l00354exon_7-361:not_in_gb_record,cholecystokinin_(cck)_gene
l43821mrna_3222-3774,enhancer_of_filamentation_(hef1)_mrna_complete_cds
all_m15517_182-
- 25 480,_ttr_gene_extracted_frommutant_prealbumin_gene_directly_linked_to_familial_amyloi
all_m17183_531-752,parathyroid_hormone-related_protein_mrna_complete_cds
all_m17466_3487-4040,blood_coagulation_factor_xii_(f12)_gene
m20642mrna_369-898,alkali_myosin_light_chainmrna_complete_cds
m69238_2033-2579,aryl_hydrocarbon_receptor_nuclear_translocator_(arnt)_mrna_complete_cds
- 30 m90299mrna_2142-2628,glucokinase_(gck)_mrna_complete_cds
s43646_1904-2402,_cytokeratin[human,_epidermis,_mrna,_2427_nt]
s77582_2-
55,_hervk10/hummtv_reverse_transcriptase_homolog_{clone_rt240}_{human,_multiple_sclerosis,_
s78798_1252-1687,_1-phosphatidylinositol-4-phosphate_5-
kinase_isoform_c_[human,_peripheral_blood_leu
- 35 s79219_344-902,_metastasis-
associated_gene_[human,_highly_metastatic_lung_cell_subline_anip[937],_mr
s82592_357-861,_evi-1=evi-
1_protein_{3'_region,_deletion_region}_{human,_megakaryoblastoid_cell_line

- u13219_1945-2473,forkhead_protein_freac-1_mrna_complete_cds_
u18549exon#2_1091-1571,gpr6_g_protein-coupled_receptor_gene_complete_cds
u40317_5400-5965,protein_tyrosine_phosphatase_ptpsigma_(ptpsigma)_mrna_complete_cds_
u49250_2323-2851,putative_cerebral_cortex_transcriptional_regulator_t-brain-1_(tbr-
5 1)_mrna_complete
u58130_2887-3301,bumetanide-sensitive_na-k-2cl_cotransporter_(nkcc2)_mrna_complete_cds
u67615_12883-13381,beige_protein_homolog_(chs)_mrna_complete_cds
u77846mrna_979-
1356,elastin_gene_partial_cds_and_partial_3'_utr,elastin_gene_partial_cds_and_parti
10 u79277_986-1520,clone_23548_mrna_sequence
u89995_3040-3460,dna_binding_protein_fkhl15_(fkhl15)_mrna_complete_cds
u92015_605-1031,clone_143789_defective_mariner_transposon_hsmar2_mrna_sequence_
all_x07876_1706-2205,mrna_for_irp_protein_(int-1_related_protein)
x16706cds_541-931:in_reversesequence,_970,fra-2_mrna
15 x54380mrna_4050-4590,mrna_for_pregnancy_zone_protein_
all_x64269_2501-2754,gene_mttf1_for_mitochondrial_transcription_factor_1_
x68561cds_2234-2324:in_reversesequence,_2547-2943,spr-1_mrna_for_gt_box_binding_protein_
all_x69920_2736-3249,mrna_for_calcitonin_receptor
all_x73079_2348-2919,encoding_polymeric_immunoglobulin_receptor_
20 all_x77737_992-1431,mrna_for_red_cell_anion_exchanger_(epb3_ael_band_3)_3'_non-
coding_region_
all_x78342_1655-1857,pisslre_mrna
x78711cds_1553-1638:in_reversesequence,_1665-1735,mrna_for_glycerol_kinase_testis_specific_1
x87871cds_939-1367:in_reversesequence,_1472-1588,mrna_for_hepatocyte_nuclear_factor_4b
25 all_x90846_2935-3407,mrna_for_mixed_lineage_kinase_2,mrna_for_mixed_lineage_kinase_2
x91220_3940-4165,mrna_for_na-cl_electroneutral_thiazide-sensitive_cotransporter
all_z11502_886-1451,mrna_for_intestine-specific_annexin
z48051mrna_1733-2303,gene_for_myelin_oligodendrocyte_glycoprotein_(mog)_
all_z70218_2-333,mrna_for_mn1_protein_(clone_icrfp507i0498)
30 all_z73903_5001-5554,mrna_for_trpc1a.
z96810cds_482-968,dna_sequence_from_pac_452h17_on_chromosome_x_contains_sodium-
and_chloride-dependen
Metagene 334
35
d13146mrna#1_2083-2551,_2',3'-cyclic-nucleotide_3'_-
phosphodiesterase_gene_extracted_from2',3'_-c
d21235_1418-1673,mrna_for_hhr23a_protein_complete_cds_
d83702_2392-2902,brain_mrna_for_photolyase_homolog_complete_cds_

- d87452_3950-4418,mrna_for_kiaa0263_gene_complete_cds
d87459_2144-2564,mrna_for_kiaa0269_gene_complete_cds
113848_3675-4161,rna_helicase_a_mrna_complete_cds_
120591exon_1-295:not_in_gb_record,annexin_iii (anx3)_gene_alternative
5 m22348_3-494,mitochondrial_ubiquinone-binding_protein_mrna_complete_cds_
s74017_1721-2213,_nrf2=nf-e2-
like_basic_leucine_zipper_transcriptional_activator_[human,hemin-induc
s75313_1197-1387,_mjd1=mjd1_protein_{cag_repeats}_[human,_brain,_mrna,_1776_nt]
u19765exon#5_630-1194,nucleic_acid_binding_protein_gene_complete_cds
10 u64105_2540-3104,guanine_nucleotide_exchange_factor_p115-rhogef_mrna_partial_cds
u67156_4641-5151,mitogen-activated_kinase_kinase_kinase(mapkkk5)_mrna_complete_cds_
all_x06318_2381-2541,mrna_for_protein_kinase_c_(pkc)_type_beta_i_
x55740mrna_2940-3516,placental_cdna_coding_for_5'_nucleotidase_(ec_3.1.3.5)
all_x76648_338-777,mrna_for_glutaredoxin_
15 z78291_28-223,mrna_(clone_1d8).

Metagene 311

- d13305_1572-1992,mrna_for_brain_cholecystokinin_receptor_
20 d55640_110-635,monocyte_pabl_(pseudoautosomal_boundary-
like_sequence)_mrna_clone_mo2/gb=d55640/_nty
119063exon_79-451,glial-
derived_neurotrophic_factor_gene_complete_cds/gb=119063/_ntype=dna/_annot=e
139211_1877-2399,mitochondrial_carnitine_palmitoyltransferase_i_mrna_complete_cds
25 m10051_4111-4651,insulin_receptor_mrna_complete_cds_
m69203cds_4-254:in_reversesequence,_122-144,cytokine_(scya2)_gene_
u03644_1050-1452,recpin_mrna_complete_cds
u17566_2214-2754,65_kda_hydrophobic_protein_mrna_complete_cds_
u78628_7-
30 199,leukemia_inhibitory_factor_receptor_mrna_5'_untranslated_region/gb=u78628/_ntype=rna_
x66363cds_1279-1459:in_reversesequence,_1594-1702,mrna_pctaire-
1_for_serine/threonine_protein_kinase
x85785mrna_1060-1498,darc_gene
x99076mrna_736-1234,nrgn_gene_exons_2,3_&(joined_cds)_
35 y00451cds_1461-1890:in_reversesequence,_2009-2037,mrna_for_5-aminolevulinate_synthase_

Metagene 175

m31661_2134-2674,prolactin_(prl)_receptor_mrna_complete_cds_

u12139exon_13-

151,alpha1(xi)_collagen_(coll1a1)_gene,_5'_region_and_exon/gb=u12139/_ntype=dna/_annot

Metagene 43

5

d11086_976-1408,mrna_for_interleukinreceptor_gamma_chain

hg2090-ht2152_s_at_hg2090-ht2152_external_membrane_protein,_130_kda

hg2639-ht2735_s_at_hg2639-ht2735_single-stranded_dna-binding_protein_mssp-1

m30257_2214-2709,vascular_cell_adhesion_moleculermrna,_complete_cds

10 m33600_581-1109,mhc_ii_hla-dr-beta-1_(hla-drb1)_mrna,_complete_cds_

m37033_915-1395,cd53_glycoprotein_mrna,_complete_cds_

m60830exon_1480-2020,evi2b3p_gene,_exon_and_complete_cds_

m83221_1788-2262,i-rel_mrna,_complete_cds_

s73813_1337-

15 1775,_cd39=lymphoid_cell_activation_antigen_[human,_b_lymphoblastoid_cell_line,_mp-1,_mr
u95626mrna#3_2792-

3278,_ccr2_gene_(ccr2a)_extracted_fromccr2b_(ccr2),_ccr2a_(ccr2),_ccr5_(ccr5)_and_

x04500exon#7_244-778,gene_for_prointerleukinbeta

x56841mrna_1269-1713,hla-e_gene

20 all_x57522_2229-2788,ring4_cdna

x64072cds_1948-2281:not_in_gb_record,_hsapiens_cd18_exon_2_

all_x99687_221-732,mrna_for_methyl-cpg-binding_protein_2,_intron/gb=x99687/_ntype=rna_

all_y00062_3996-4597,mrna_for_t200_leukocyte_common_antigen_(cd45,_lc-a)_

y09561cds_1238-1676:in_reversesequence,_1798,mrna_for_p2x7_receptor_

25 z14982mrna#1_616-1150,_mhc-encoded_proteasome_subunit_gene_lamp7-
e1_gene_(proteasome_subunit_lmp7)_e

Metagene 458

30 hg2339-ht2435_at_hg2339-ht2435_nuclear_factor_1,_variant_hepatic_

l11702_2837-3335,phospholipase_d_mrna,_complete_cds

l38820exon_170-620,hmc_i_antigen-like_glycoprotein_(cd1d)_gene

m93119_2345-2777,zinc-finger_dna-binding_motifs_(ia-1)_mrna,_complete_cds

all_u34301_1497-

35 1528,nonmuscle_myosin_heavy_chain_iib_gene,_promoter_region_and_exon/gb=u34301/_ntyp
u66497_3549-4047,leptin_receptor_splice_variant_form_13.2_mrna,_complete_cds.

u73191_1078-1582,inward_rectifier_potassium_channel_(kir1.3),_complete_cds_

all_x75756_3248-3699,mrna_for_protein_kinase_c_mu

Metagene 222

- d87444_3517-3823,mrna_for_kiaa0255_gene,_complete_cds
d89859_2331-2841,mrna_for_zinc_fingerprotein,_complete_cds
- 5 hg162-ht3165_at_hg162-ht3165_tyrosine_kinase_receptor_axl,_altsplice_2
hg33-ht33_at_hg33-ht33_ribosomal_protein_s4,_x-linked
l06147_1586-2042,(clone_sy11)_golgin-95_mrna,_complete_cds_
l10910_2084-2552,splicing_factor_(cc1.3)_mrna,_complete_cds_
m18737mrna_269-
- 10 815,_gjalp1_gene_extracted_fromhanukah_factor_serine_protease_(huhf)_mrna,_complete_c
all_m29277_2842-
2926,isolate_juso_muc18_glycoprotein_mrna_(3'_variant),_complete_cds,isolate_juso_mu
m33493_504-792,tryptase-iii_mrna,_3'_end_
m83822_6791-7253,beige-like_protein_(bgl)_mrna,_partial_cds
- 15 s52969_cds1_s_at_s52969_s52969,not_in_gb_record,_description:_alpha-
1,3_fucosyltransferase_gene_extr
u07620_1861-2215,map_kinase_mrna,_complete_cds_
u48705mrna_3326-3867,receptor_tyrosine_kinase_ddr_gene,_complete_cds
u63295_1285-1795,seven_in_absentia_homolog_mrna,_complete_cds
- 20 u67122_469-728,ubiquitin-related_protein_sumo-1_mrna,_complete_cds.
u70660_31-463,copper_transport_protein_hah1_(hah1)_mrna,_complete_cds
x80907_2095-2557,mrna_for_p85_beta_subunit_of_phosphatidylinositol-3-kinase_
x84707mrna_73-511,mia_gene
x89211cds_1571-
- 25 2129,dna_for_endogenous_retroviral_like_element/gb=x89211/_ntype=dna/_annot=cds_
all_z21966_1647-2182,mpou_homeobox_protein_mrna
z36715cds_1026-1200:in_reversesequence,_1491-1557,mrna_for_net_transcription_factor_

Metagene 249

- 30 m15780cds_13-
304,dna/endogenouspapillomavirus_type(hpv)_dna,_right_flank_and_viral_host_junction/gb=
m22092exon_6-42,neural_cell_adhesion_molecule_(n-
cam)_gene,_exon_sec_and_partial_cds/gb=m22092/_ntyp
- 35 u18004_31-205,_hsu18004cdna_

Metagene 432

- ac002115_66940-67151:in_ac002115cds#2_675-
 1000_cox6b_gene_(coxg)_extracted_fromdna_from_overlapping
 hg371-ht26388_s_at_hg371-ht26388_mucin_1_epithelial_altsplice_9
 j05252_1611-2178,kex2-like_endoprotease_mrna_complete_cds.
- 5** j05556mrna_1640-2198,collagenase_mrna_complete_cds_
 all_m18255_18-408:in_m18255cds_47_prkacb_gene_(protein_kinase_c-beta-
 2)_extracted_fromprotein_kinas
 m60614_1996-2060,wilms_tumor_(wit-1)_associated_protein_mrna_complete_cds_
 s75213_1727-2087_type-iva_cyclic_amp_specific_phosphodiesterase_hpde4a_human_t-
 cells_mrna_partia
- 10** u00954_738-1224,clone_ce29_7.2_(cac)n/(gtg)n_repeat-containing_mrna
 u38904_1210-1744,zinc_finger_protein_c2h2-25_mrna_complete_cds
 u45976_1748-
 2210,clathrin_assembly_protein_lymphoid_myeloid_leukemia_(calm)_mrna_complete_cds_
 u52682_4755-
- 15** 5241,lymphocyte_specific_interferon_regulatory_factor/interferon_regulatory_factor(lsirf
 u58096_798-1056,testis-specific_protein_(tspy)_mrna_complete_cds
 u65406mrna#1_1860-2370_kcnj1_gene_(potassium_channel_rom-
 k3)_extracted_fromalternatively_spliced_po
- 20** u71203_339-753,rit_mrna_complete_cds
 u89336exon#13_173-
 695_unknown_gene_extracted_fromhla_iii_region_containing_notch4_gene_partial_seq
 all_x16660_1795-2049_open_reading_frame_p25_(aa_1-223)_gene_extracted_fromhltv-
 i_related_endogenous
- 25** x71877cds_587-767:in_reversesequence_783-1089,mrna_for_chymotrypsin-like_protease_ctrl-1
 all_x89894_2017-2486,mrna_for_nuclear_receptor_
 x93498mrna_589-1117,mrna_for_21-glutamic_acid-rich_protein_(21-garp)_
 x93512cds_61-157:in_reversesequence_175-211,mrna_for_telomeric_dna_binding_protein_(orf2)
 y00067mrna_2655-3207,gene_for_neurofilament_subunit_m_(nf-m)
- 30** y10262cds_1163-1693,eya3_gene/gb=y10262_/ntype=dna_/annot=cds
- Metagene 453
- d16481_1438-1942,mrna_for_mitochondrial_3-ketoacyl-coa_thiolase_beta-
 subunit_of_trifunctional_protei
- 35** d50914_1543-2077,mrna_for_kiaa0124_gene_partial_cds_
 d82060_1801-
 2215,kidney_mrna_for_putative_membrane_protein_with_histidine_rich_charge_clusters_comp
 d83778_4662-5154,mrna_for_kiaa0194_gene_partial_cds_

- d87443_5442-5988,mrna_for_kiaa0254_gene,_complete_cds
hg1400-ht1400_s_at_hg1400-ht1400_carboxyl_methyltransferase,_aspartate,_altsplice_1
hg2463-ht2559_at_hg2463-ht2559_guanine_nucleotide-binding_protein_g25k_
l06845_1728-2268,cysteinyI-trna_synthetase_mrna,_partial_cds_
5 l13278_1231-1753,zeta-crystallin/quinone_reductase_mrna,_complete_cds_
l13773_8844-9252,af-4_mrna,_complete_cds_
l21954exon_36-384:not_in_gb_record,peripheral_benzodiazepine_receptor_gene
l25085_103-361,sec61-complex_beta-subunit_mrna,_complete_cds_
l38961_1919-2429,putative_transmembrane_protein_precursor_(b5)_mrna,_complete_cds
10 l42572mrna_2192-2648,p87/89_gene,_complete_cds
m14200mrna_139-469,diazepam_binding_inhibitor_(dbi)_mrna,_complete_cds
m24400mrna_282-840,chymotrypsinogen_mrna,_complete_cds_
m31899_2318-2708,dna_repair_helicase_(ercc3)_mrna,_complete_cds
m64992_741-1185,prosomeal_protein_p30-33k_(pros-30)_mrna,_complete_cds
15 m65131mrna_2187-2709,methylmalonyl-coa_mutase_(mcm)_mrna,_complete_cds
m73547_2649-3153,polyposis_locus_(dpl_gene)_mrna,_complete_cds_
m83233_3488-3974,transcription_factor_(htf4a)_mrna,_complete_cds
s74728_1245-1773,_antiquitin=26g_turgor_protein_homolog_[human,_kidney,_mrna,_1809_nt]
s78569_5723-6161,_laminin_alpha_hchain_[human,_fetal_lung,_mrna,_6204_nt]
20 u10117mrna_474-954,endothelial-monocyte_activating_polypeptide_ii_mrna,_complete_cds_
u10439_5983-6529,double-stranded_rna_adenosine_deaminase_mrna,_complete_cds
u12535_3273-
3783,epidermal_growth_factor_receptor_kinase_substrate_(eps8)_mrna,_complete_cds_
u14193_135-687,tfia_gamma_subunit_mrna,_complete_cds
25 u15009_25-541,snrnp_core_protein_sm_d3_mrna,_complete_cds
u26312_166-686,heterochromatin_protein_hplhs-gamma_mrna,_complete_cds
u28686_973-1486,putative_rna_binding_protein_rnpl_mrna,_complete_cds_
u41654_1159-1525,adenovirus_protein_e3-14.7k_interacting_protein(fip-1)_mrna,_complete_cds
u41740_7119-7635,trans-golgi_p230_mrna,_complete_cds_
30 u43899_2320-2740,signal_transducing_adaptor_molecule_stam_mrna,_complete_cds_
u50523_858-1344,brca2_region,_mrna_sequence_cg037
u50950_1546-2074,infant_brain_unknown_product_mrna,_complete_cds_
u57099_666-1158,apeg-1_mrna,_complete_cds
u67319_2133-2529,lice2_beta_cysteine_protease_mrna,_complete_cds.
35 u69645_551-1037,zinc_finger_protein_mrna,_complete_cds_
u70987_1308-1830,gap_binding_protein_p62dok_(dok)_mrna,_complete_cds_
u93237mrna#1_2162-
2738,_men1_gene_(menin)_extracted_frommenin_(men1)_gene,_complete_cds.
all_x12791_311-870,mrna_for_19kd_protein_of_signal_recognition_particle_(srp)

- x52151cds_1148-1394:in_reversesequence, 1884-1980,arylsulphatase_a_mrna,_complete_cds
x52730mrna#1_455-911,_phenylethanolamine_n-
methyltransferase_gene_extracted_fromgene_for_phenylethan
x54326cds_4149-4299:in_reversesequence, 4363-4507,mrna_for_glutaminyl-trna_synthetase_
- 5 all_x63469_962-1467,mrna_for_transcription_factor_tfiie_beta_
all_x65644_8589-9100,mrna_mbp-2_for_mhc_binding_protein_2
x75535exon#8_2216-2768,mrna_for_pxf_protein
all_x75962_913-1340,mrna_for_ox40_homologue
all_x77548_2835-3418,_hsapiens_cdna_for_rfg_
- 10 all_x84195_230-723,mrna_for_acylphosphatase,_muscle_type_(mt)_isoenzyme
x99296exon#1_28-
223,_rd_fromrd_gene_(5'_partial)_and_g11a_gene_(5'_partial)/gb=x99296_/ntype=dna_/an
all_y00264_2984-3321,mrna_for_amyloid_a4_precursor_of_alzheimer_disease
all_z22551_4012-4595,kinectin_gene_
- 15 z46973cds_2460-2634:in_reversesequence, 2711-2891,mrna_for_phosphatidylinositol_3-kinase
z97074_852-1176,mrna_for_rab9_effector_p40,_complete_cds
- Metagene 415
- 20 d83657exon#1-3_13-167:in_reversesequence, 2025:not_in_gb_record,dna_for_caaf1_(calcium-
binding_prote
hg4740-ht5187_at_hg4740-ht5187_transcription_factor_eb_
m64925_1400-1940,palmitoylated_erythrocyte_membrane_protein_(mpp1)_mrna,_complete_cds
u18088_1188-1742,3',5'-
- 25 cyclic_amp_phosphodiesterase_inactive_splice_variant_hspde4a8a_mrna,_comple
u22377_5634-6168,zn-15_related_zinc_finger_protein_(rlf)_mrna,_complete_cds
u41766_3235-3653,metalloprotease/disintegrin/cysteine-
rich_protein_precursor_(mdc9)_mrna,_complete_c
u43185_3667-4243,signal_transducer_and_activator_of_transcription_stat5a_mrna,_complete_cds
- 30 u53476_841-1351,proto-oncogene_wnt7a_mrna,_complete_cds
v00536mrna_811-1135,_ifng_gene_extracted_fromimmune_interferon_(ifn-gamma)_gene_
y00282cds_1657-1849:in_reversesequence, 2341-2383,mrna_for_ribophorin_ii
- Metagene 257
- 35 ac002115cds#4_474-750:in_reversesequence, 100047-
100269,_cox6b_gene_(coxg)_extracted_fromdna_from_ov
af001620_1478-2000,trabecular_meshwork-
induced_glucocorticoid_response_protein_(tigr)_mrna,_complete

- hg4185-ht4455_at hg4185-ht4455_estrogen_sulfotransferase_ste
hg537-ht537_at hg537-ht537_collagen_type_viii_alpha_2
119183mrna_1533-1959,mac30_mrna,_3'_end
127584cds_1093-1400:in_reversesequence,_1464-
- 5** 1677,ca_channel_b3_subunit(cal_bet_3)_mrna,_complete_c
139009mrna_109-
475,iv_alcohol_dehydrogenase(adh7)_gene,_5'_flanking_region/gb=l39009_/ntype=dna_/ann
m10058mrna_706-1252,asialoglycoprotein_receptor_h1_mrna,_complete_cds
m18700cds_288-784,elastase_iii_a_gene,_exon_8
- 10** m24122mrna_309-774,myosin_alkali_light_chain_(ventricular)_mrna,_complete_cds
m26679exon#2_505-925,homeobox_protein(hox-1.3)_gene,_complete_cds
m73047_4025-4565,tripectidyl_peptidase_ii_mrna,_complete_cds
s67156_876-1368,_asp=aspartoacylase_[human,kidney,mrna,_1435_nt]
u07225_1430-1958,p2u_nucleotide_receptor_mrna,_complete_cds
- 15** u18288_2804-3314,clone_ciita-10_mhc_ii_transactivator_ciita_mrna,_complete_cds_
u19878_1137-1647,transmembrane_protein_mrna,_complete_cds
x52479cds_1689-1995:in_reversesequence,_2040-
2202,pkc_alpha_mrna_for_protein_kinase_c_alpha_
x99802_1983-2463,mrna_for_zyg_homologue
- 20** z33642mrna_2763-3291,v7_mrna_for_leukocyte_surface_protein_

Metagene 321
- all_d13315_1488-1975,mrna_for_lactoyl_glutathione_lyase
- 25** d14812_1345-1747,mrna_for_kiaa0026_gene,_complete_cds
d16469_2264-2738,mrna_for_orf_xq_terminal_portion_
d23662_61-565,mrna_for_ubiquitin-like_protein,_complete_cds
d30756_4053-4611,mrna_for_kiaa0049_gene,_complete_cds
d31767_1338-1812,mrna_for_kiaa0058_gene,_complete_cds
- 30** d50495mrna_493-1033,mrna_for_transcription_elongation_factor_s-ii,_hs-ii-t1,_complete_cds
d86985_5502-5946,mrna_for_kiaa0232_gene,_complete_cds
d87438_3322-3808,mrna_for_kiaa0251_gene,_partial_cds_
hg1595-ht4788_s_at hg1595-ht4788_heterogeneous_nuclear_ribonucleoprotein_i,_altsplice_2,_ptb-
1_
- 35** hg4683-ht5108_s_at hg4683-ht5108_tumor_necrosis_factor_receptorassociated_protein_trap3_
hg998-ht998_s_at hg998-ht998_sulfotransferase,_phenol-preferring_
j03805_926-1491,phosphatase_2a_mrna,_partial_cds_
l19686mrna_61-493,macrophage_migration_inhibitory_factor(mif)_gene,_complete_cds
l36151_2433-2907,phosphatidylinositol_4-kinase_mrna,_complete_cds_

- l38810mrna_706-1246,thyroid_receptor_interactor_(trip1)_mrna,_complete_cds
 l40391mrna_889-1435,(clone_s153)_mrna_fragment
 l43964_1671-2211,(clone_f-t03796)_stm-2_mrna,_complete_cds
 l77213mrna_479-959,phosphomevalonate_kinase_mrna,_complete_cds
- 5** m34175mrna_5100-5670,beta_adaptin_mrna,_complete_cds_
 m62762_681-1083,vacuolar_h+_atpase_proton_channel_subunit_mrna,_complete_cds_
 m63959_1030-1444,alpha-2-macroglobulin_receptor-associated_protein_mrna,_complete_cds
 m69023_524-1088,globin_gene
 m98343_2695-3163,amplaxin_(ems1)_mrna,_complete_cds_
- 10** u02556_1579-2101,rp3_mrna,_complete_cds
 u17969exon#6_165-663,initiation_factor_eif-5a_gene,_complete_cds_
 u19796_406-760,melanoma_antigen_p15_mrna,_complete_cds_
 u22897_1798-2338,nuclear_domainprotein_(ndp52)_mrna,_complete_cds_
 u25435_3227-3737,transcriptional_repressor_(ctcf)_mrna,_complete_cds_
- 15** u31930_411-963,deoxyuridine_nucleotidohydrolase_mrna,_complete_cds_
 u36341mrna#1_3376-
 3862,_slc6a8_gene_(creatine_transporter)_extracted_fromxq28_cosmid,_creatine_trans
 u49869mrna_785-887,ubiquitin_gene,_complete_cds_
 u64444_633-1113,ubiquitin_fusion-degradation_protein_(ufd11)_mrna,_complete_cds
- 20** u72342mrna_5025-
 5499,platelet_activating_factor_acetylhydrolase,_brain_isoform,_45_kda_subunit_(lis1
 u78095_942-1434,placental_bikunin_mrna,_complete_cds_
 u80017mrna#2_5760-
 6039,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcripti
- 25** u81556_1541-1925,hypothetical_protein_a4_mrna,_complete_cds
 all_x04526_2577-2968,liver_mrna_for_beta-subunit_signal_transducing_proteins_gs/gi_(beta-g)
 x13546mrna_657-1137,_puthmg-17_protein_gene_extracted_fromhmg-17_gene_for_non-
 histone_chromosomal_pr
 x15341cds_13-235:in_reversesequence,_374-500,cox_via-1_mrna_for_cytochrome_c_oxidase_liver-
 specific_
- 30** all_x55330_1609-2120,mrna_for_aspartylglucosaminidase
 x56681mrna_1311-1835,jund_mrna_
 all_x64330_3792-4243,mrna_for_atp-citrate_lyase
 all_x64364_1014-1561,mrna_for_m6_antigen_
- 35** all_x75593_679-1202,mrna_for_rab_13
 x82103cds_660-840:in_reversesequence,_954-1128,mrna_for_beta-cop
 all_x84709_1088-1683,mrna_for_mediator_of_receptor-induced_toxicity
 z35093cds_674-842:in_reversesequence,_898-976,mrna_for_surf-1_

Metagene 473

j00219cds_110-467:in_reversesequence,_4721-4823,immune_interferon_(ifn-gamma)_gene,_complete_cds

5

s78873_291-

835,_mss4=zn2+_binding_protein/guanine_nucleotide_exchange_factor_[human,_brain,_mrna_parallel_s83366_910-

2840,_region_centromeric_to_t(12;17)_breakpoint:_orf1/unknown_43_amino_acid_transcript_y10515mrna_79-307,mrna_for_cd58_t7_protein/gb=y10515/_ntype=ma

10

z83800_115-505,mrna_for_cytoplasmic_dynein_heavy_chain_(partial,_id_hdhc11)

Metagene 470

d49677_905-1445,u2af1-rs2_mrna,_complete_cds_

15

hg2797-ht2905_s_at_hg2797-ht2905_clathrin,_light_polypeptide_altsplice_1

l22548_2914-3334,collagen_type_xviii_alpha(col18a1)_mrna,_partial_cds_

l27624_373-917,tissue_factor_pathway_inhibitor-2_mrna,_complete_cds_

m57710_355-865,ige-binding_protein_(epsilon-bp)_mrna,_complete_cds_

s54005_2-197,_thymosin_beta-10_[human,_metastatic_melanoma_cell_line,_mrna,_453_nt]_

20

s75295_2339-

2915,_nucleoprotein_interactor_1=srp1_homolog_[human,_cervical_carcinoma_hela_cells,_mrna_s81578_13-271,_dioxin-

responsive_gene_{putative_polyadenylation_signal_region}_[human,_hepatoma_g2_c

u09410_1481-2003,zinc_finger_protein_znf131_mrna,_partial_cds

25

u26648_936-1482,syntaxinmrna,_complete_cds

u46025cds_2254-2710:in_reversesequence,_2777-2843,translation_initiation_factor_eif-3_p110_subunit_g

all_x57348_844-1377,mrna_(clone_9112)

all_x66087_3046-3563,a-myb_mrna

30

all_x69433_1312-1733,mrna_for_mitochondrial_isocitrate_dehydrogenase_(nadp+)_

x70476mrna_2526-3024,subunit_of_coatomer_complex_

x98507cds_2790-3018:in_reversesequence,_3131-3293,mrna_for_myosin-i_beta

y08136cds_292-496:in_reversesequence,_520-820,mrna_for_asm-like_phosphodiesterase_3a

35

Metagene 462

d88155cds_1025-1357:in_reversesequence,_439-576,dna_for_ad4bp_(sf-1)_gene_

hg3925-ht4195_at_hg3925-ht4195_surfactant_protein_sp-a2_delta_

- j02960cds#1_394-729:in_reversesequence,_1015-
 1252,unknown_protein_gene_extracted_frombeta-2-adrener
 178833exon#24_1038-
 1476,brcal_gene_extracted_frombrcal_rho7_and_vati_genes_complete_cds_and_ipf3
- 5** m16937_806-1310,homeo_box_c1_protein_mrna_complete_cds_
 all_m21064_1360-1426,migration_inhibitory_factor-related_protein(mrp14)_gene_complete_cds_
 m76558_7124-7592,neuronal_dhp-sensitive_voltage-dependent_calcium_channel_alpha-
 1d_subunit_mrna_c
 u18548exon_620-1046,gpr12_g_protein_coupled-receptor_gene_complete_cds
- 10** u29195exon_927-1443,neuronal_pentraxin_ii_(nptx2)_gene_
 u32324_1353-1671,interleukin-11_receptor_alpha_chain_mrna_complete_cds
 u92027_524-1028,clone_61501_defective_mariner_transposon_hsmar2_mrna_sequence
 all_x15218_3012-3511,ski_oncogene_mrna_
 x51954exon_10-148,ucp_gene_for_uncoupling_protein_exon/gb=x51954_/ntype=dna_/annot=exon_
- 15** x52282cds_1092-1597,mrna_for_atrial_natriuretic_peptide_clearance_receptor_(anp-c_receptor)
 all_x96698_662-1245,mrna_for_d1075-like_gene_
 y09615cds_891-1131:in_reversesequence,_1268-
 1472,mrna_for_mitochondrial_transcription_termination_fa
 y13618_7553-7895,mrna_for_dffry_protein_abundant_transcript
- 20** z73677mrna_91-137,gene_encoding_plakophilin_1b.
- Metagene 445
- ab002314_6334-6898,mrna_for_kiaa0316_gene_complete_cds/gb=ab002314_/ntype=rna_
25 hg2600-ht2696_at_hg2600-ht2696_guanine_nucleotide-binding_protein_rap2b_ras-
 oncogene_related
 hg2602-ht2698_at_hg2602-ht2698_succinate_dehydrogenase_flavoprotein_subunit_
 l27586_1755-2205,tr4_orphan_receptor_mrna_complete_cds
 all_m24748_1170-1531_thral_gene_(thyroid_receptor_alpha-
30 1)_extracted_fromthyroid_hormone_receptor_a
 u45983cds_789-1005:in_reversesequence,_1304-1496,g_protein-coupled_receptor_gpr-
 cy6_gene_complete_c
 u49187_1780-2206,placenta_(diff48)_mrna_complete_cds
 u66464_2131-2701,hematopoietic_progenitor_kinase_(hpk1)_mrna_complete_cds_
35 u70321_1127-1643,herpesvirus_entry_mediator_mrna_complete_cds_
 x66360cds_1134-1518:in_reversesequence,_1629-1689,mrna_pctaire-
 2_for_serine/threonine_protein_kinase
 all_x90840_6383-6942,mrna_for_axonal_transporter_of_synaptic_vesicles
 all_z80777_449-807,h2a/k_gene

Metagene 442

- hg2075-ht2137_s_at_hg2075-ht2137_camp-responsive_element_modulator,_altsplice_1
- 5 m30135cds_139-361:in_reversesequence,_4255-4303,p40_t-
cell_and_mast_cell_growth_factor_(hp40)_gene,_
u13680_767-1160,lactate_dehydrogenase-c_(ldh-c)_mrna,_complete_cds_
u66033_1937-2495,glypican-5_(gpc5)_mrna,_complete_cds
all_x51420_2264-2781,mrna_for_tyrosinase-related_protein_
10 x58298cds_824-1371:in_reversesequence,_1441,mrna_for_interleukin-6-receptor_

Metagene 425

- ab000410mrna_947-1442,hogg1_mrna,_complete_cds_
15 d13118_61-523:in_reversesequence,_529,mrna_for_atp_synthase_subunit_c_encoded_by_p1_gene
d16611_1726-2299,mrna_for_coproporphyrinogen_oxidase,_complete_cds_
d85418_875-1403,mrna_for_phosphatidylinositol-glycan-class_c_(pig-c),_complete_cds_
d86519_1368-1932,mrna_for_neuropeptide_y/peptide_yy_y6_receptor,_complete_cds
d87845_1946-2216,mrna_for_platelet-activating_factor_acetylhydrolase_2,_complete_cds_
20 hg3491-ht3685_at_hg3491-ht3685_zinc_finger_protein_zfp-36
j03925_4110-4656,mac-1_gene_encoding_complement_receptor_type_3,_cd11b,_complete_cds_
j04970_1397-1715,carboxypeptidase_m,_3' end
114595_1801-2077,alanine/serine/cysteine/threonine_transporter_(asct1)_mrna,_complete_cds
l34657mrna_2757-3219,platelet/endothelial_cell_adhesion_molecule-1_(pecam-1)_gene_
25 m28212_175-691,gtp-binding_protein_(rab6)_mrna,_complete_cds
m55543mrna_1356-1872,guanylate_binding_protein_isoform_ii_(gbp-2)_mrna,_complete_cds_
m55683_2732-3242,cartilage_matrix_protein_(cmp)_mrna,_exons_8-mar
m62424_2868-3117,thrombin_receptor_mrna,_complete_cds
m63154_977-1541,intrinsic_factor_mrna,_complete_cds
30 m95809_1310-1850,basic_transcription_factor_62kd_subunit_(btf2),_complete_cds
s83249_19-349,_ng-
tra=transporter_protein/putative_hormone_extrusion_pump_[human,_liver_and_various_
u03270_626-1136,centrin_mrna,_complete_cds_
u20938_3946-4348,lymphocyte_dihydropyrimidine_dehydrogenase_mrna,_complete_cds.
35 u40992_839-1175,heat_shock_protein_hsp40_homolog_mrna,_complete_cds
u68133_4-133,scc-
s4_mrna_expressed_in_primary_and_relatively_radiosensitive_squamous_cell_carcinoma,
u88667_6771-7251,atp_binding_cassette_transporter_(abcr)_mrna,_complete_cds
all_x00088_334-787,histone_h2b_gene

all_x67081_578-810,histone_h4_gene_
 x69089_4333-4849,mrna_for_skeletal_muscle_165kd_protein
 x89101exon#3_8-96:in_reversesequence,_183-188,mrna_for_fas_(apo-
 1_cd95)/gb=x89101_/ntype=rna_

- 5** x90530cds_632-1100:in_reversesequence,_1548-1554,mrna_for_ragb_protein
 z68747cds_656-1106:in_reversesequence,_1177,mrna_for_imogen_38
 z69915mrna_31-244,mrna_(clone_icrfp50711876).

Metagene 389

10

j05125_1038-1422,triglyceride_lipase_mrna,_complete_cds
 m68840_1558-1924,monoamine_oxidase_a_(maoa)_mrna,_complete_cds_
 u85707_1922-2426,leukemogenic_homolog_protein_(meis1)_mrna,_complete_cds_
 u90916_1309-1825,clone_23815_mrna_sequence_

15

Metagene 363

hg1496-ht1496_s_at_hg1496-ht1496_adrenal-specific_protein_pg2
 s73205_2183-

- 20** 2573,_insulin_activator_factor_[human,_pancreatic_insulinoma,_mrna_partial,_2622_nt]/gb=
 u00930_2705-3191,clone_c4e_1.63_(cac)n/(gtg)n_repeat-containing_mrna_
 x59131_2735-3119:not_in_gb_record,d13s106_mrna_for_a_highly_charged_amino_acid_sequene

Metagene 350

25

d14497_2222-2726,mrna_for_proto-oncogene_protein,_complete_cds_
 d64015_1126-1222,mrna_for_t-cluster_binding_protein,_complete_cds/gb=d64015_/ntype=rna
 l00352exon_1952-2492,low_density_lipoprotein_receptor_gene_
 l07493_193-631,replication_protein_a_14kda_subunit_(rpa)_mrna,_complete_cds_
30 u20980_1596-2118,chromatin_assembly_factor-i_p60_subunit_mrna,_complete_cds
 u34962_1074-1560,transcription_factor_hcsx_(hcsx)_mrna,_complete_cds_
 u46571_1183-1687,tetratricopeptide_repeat_protein_(tpr2)_mrna,_complete_cds
 x56088mrna_2240-2794,mrna_for_cholesterol_7-alpha-hydroxylase

35 Metagene 344

m57293mrna#1_4-289,parathyroid_hormone-
 related_peptide_(pthrp)_gene,_exons_1a,_1b,_1c,_and/gb=m57293
 m85276exon#2-5_5-92:in_reversesequence,_5295:not_in_gb_record,nkg5_gene,_complete_cds_

all_x69116_2-434,znf37a_gene_for_zinc_finger_protein_
z80345mrna_4931-5457,scad_gene,_5'_utr_exonand(and_joined_cds)

Metagene 315

5

d83018_2645-3149,mrna_for_nel-related_protein_2,_complete_cds
all_l31860_2084-2589,glycophorin_mn-types_(gypa)_mrna,_complete_cds_
m16961_937-1477,alpha-2-hs-glycoprotein_alpha_and_beta_chain_mrna,_complete_cds
all_u01317_19502-63478,_epsilon-
10 globin_gene_extracted_frombeta_globin_region_on_chromosome_11,_epsil
u01877_8517-8997,p300_protein_mrna,_complete_cds_

Metagene 314

- 15 104656_370-856,carbonic_anhydrase_related_protein_(carp)_mrna,_complete_cds_
149209exon_25-
92,retinoblastoma_susceptibility_protein_(rb1)_i66dbp_deletion_mutant_(resulting_in_pr
m84605_4280-4766,putative_opioid_receptor_mrna,_complete_cds_
u14747_410-944,visinin-like_peptidehomolog_mrna,_complete_cds_
20 u21556_709-1204,membrane_protein-like_protein_mrna,_partial_cds/gb=u21556_/ntype=rna_
u50929_1910-2330,betaine:homocysteine_methyltransferase_mrna,_complete_cds_
u83326cds_538-1010,cc_chemokine_receptor-5_(ccr5)_gene,_complete_cds.

Metagene 259

25

m57471exon_13-59,urate_oxidase_(uox)_gene,_exon/gb=m57471_/ntype=dna_/annot=exon_
m99439_1082-1385,transducin-like_enhancer_protein_(tle4)_mrna,_3'_end
u46024_2801-3377,myotubularin_(mtm1)_mrna,_partial_cds_
all_u57341_2-
30 129,neurofilament_triplet_1_protein_mrna,_partial_cds/gb=u57341_/ntype=rna,neurofilamen
u82468_1566-2091,tubby_related_protein(tulp1)_mrna,_complete_cds
x56741cds_85-595:in_reversesequence,_617,mrna_for_rab8_gene_
x74328mrna_1175-
1745,_cb2_(peripheral)_cannabinoid_receptor_gene_extracted_frommrna_for_cb2_(periphe

35

Metagene 232

all_d38024_2639-
3228,facioscapulohumeral_muscular_dystrophy_(fshd)_gene_region,_d4z4_tandem_repeat_u

hg2260-ht2349_s_at_hg2260-ht2349_duchenne_muscular_dystrophy_protein_(dmd)_
 hg4020-ht4290_s_at_hg4020-ht4290_transglutaminase
 m13994mrna_4482-5005,b-cell_leukemia/lymphoma(bcl-2)_proto-oncogene_mrna_encoding_bcl-2-
 alpha_protei

- 5 u27516_2109-2555,recombination_protein_rad52_mrna,_complete_cds
 u82970_2601-3009,metalloendopeptidase_homolog_(pex)_mrna,_complete_sequence
 x03168cds_926-1400:in_reversesequence,_1497-1509,mrna_for_s-protein_
 all_x89067_751-1136,mrna_for_trpc2_transcript_(possible_pseudogene)

10 Metagene 226

ab001325_967-1387,aqp3_gene_for_aquaporine(water_channel),_partail_cds
 all_d31784_3804-4249,mrna_for_cadherin-6_
 d42087_1034-1388,mrna_for_kiaa0118_gene,_partial_cds_

- 15 d87436_5660-6116,mrna_for_kiaa0249_gene,_complete_cds
 all_132866_67-452,effector_cell_protease_receptor-1_(epr-1)_gene,_partial_cds
 all_m17262_16806-
 26862:in_m17262cds_1666,prothrombin_(f2)_gene,_complete_cds,_and_alu_and_kpni_repea
 m26692exon#1_37-195,lymphocyte-

- 20 specific_protein_tyrosine_kinase_(lck)_gene,_exon_1,_and_downstream_p
 m30269_4417-4849,nidogen_mrna,_complete_cds
 s55606_718-1228,_betacellulin_[human,_mrna,_1271_nt]
 u02019_1958-2462,au-rich_element_rna-binding_protein_auf1_mrna,_complete_cds_
 u18934_4229-4311,receptor_tyrosine_kinase_(dtk)_mrna,_complete_cds_

- 25 u58034cds_38-
 224,myotubularin_related_protein(mtmr3)_gene,_partial_cds/gb=u58034_/ntype=rna_
 u79246_1346-1748,clone_23799_mrna_sequence_
 u79289_1287-1809,clone_23695_mrna_sequence_
 x71125utr#1_20-398:in_reversesequence,_985-1093,mrna_for_glutamine_cyclotransferase_
 30 all_x97261_25-333,mrna_for_metallothionein_isoform_1r,mrna_for_metallothionein_isoform_1r_
 x97674cds_4092-4326:in_reversesequence,_4536-
 4758,mrna_for_transcriptional_intermediary_factor_2

Metagene 188

35

d10537_1359-1876,mrna_for_major_structural_protein_of_myelin,_complete_cds_
 d26443_3282-3822,mrna_for_glutamate_transporter,_complete_cds
 d31897_1050-1548,mrna_for_doc2_(double_c2),_complete_cds_
 d38081_2769-2853,mrna_for_thromboxane_a2_receptor,_complete_cds

- d43767_43-505,mrna_for_chemokine,_complete_cds_
d50855_2772-3309,mrna_for_ca-sensing_receptor,_complete_cds_
d63940_153-656,mrna_for_mx11_protein,_complete_cds_
d80007_5240-5768,mrna_for_kiaa0185_gene,_partial_cds_
5 d82344_2434-2986,mrna_for_nbphox,_complete_cds_
d89501exon#3_206-441,pbi_gene,_complete_cds
hg3405-ht3586_at_hg3405-ht3586_zinc_finger_protein_hzf3
hg3495-ht3689_at_hg3495-ht3689_collagen,_type_ix,_alpha_1
hg358-ht358_at_hg358-ht358_homeotic_protein_7,_notch_group_
10 hg3921-ht4191_f_at_hg3921-ht4191_homeotic_protein_c6,_i
hg3962-ht4232_at_hg3962-ht4232_sialyltransferase,_stx
hg4069-ht4339_s_at_hg4069-ht4339_monocyte_chemotactic_protein_
hg4318-ht4588_s_at_hg4318-ht4588_lim-domain_transcription_factor_lim-1_
107738_717-1125,dhp-sensitive_calcium_channel_gamma_subunit_(cacnlg)_mrna,_complete_cds_
15 107765_1443-1923,carboxylesterase_mrna,_complete_cds_
110403_834-1254,dna_binding_protein_for_surfactant_protein_b_mrna,_complete_cds_
131881_929-1385,nuclear_factor_i-x_mrna,_complete_cds
138517mrna_766-1228,indian_hedgehog_protein_(ihh)_mrna,_5'_end
143338mrna_25-151,(clone_jj1a)_cadherin_mrna_fragment/gb=143338/_ntype=ma
20 143366mrna_13-157,(clone_jj1b)_cadherin_mrna_fragment/gb=143366/_ntype=ma
m15059mrna_1025-1487,fc-epsilon_receptor_(ige_receptor)_mrna,_complete_cds_(h107_epitope)
all_m19878_1799-
1946,calbindin_27_gene,_exonsand_2,_and_alu_repeat/gb=m19878/_ntype=dna/_annot=exon,
m20203cds_242-364,neutrophil_elastase_gene_
25 m55047_2637-3207,synaptotagmin_mrna,_complete_cds
m55067_754-1324,47-kd_autosomal_chronic_granulomatous_disease_protein_mrna,_complete_cds_
m59488mrna_536-1016,s100_protein_beta-subunit_gene_
all_m60752_611-863,histone_h2a.1_(h2a)_gene,_complete_cds
m64676mrna_1619-1892,k+_channel_subunit_gene,_complete_cds_
30 m80647_1317-1857,thromboxane_synthase_mrna,_complete_cds
m84371mrna_1318-1824,cd19_gene,_complete_cds
m85247mrna_141-
597,dopamine_d1a_receptor_gene,_complete_exon_1,_and_exon_2,_5'_end/gb=m85247/_ntype=
all_m86528_954-1357,neurotrophin-4_(nt-4)_gene,_complete_cds_
35 m97639_3533-4037,transmembrane_receptor_(ror2)_mrna,_complete_cds
m97675_2799-3309,transmembrane_receptor_(ror1)_mrna,_complete_cds
m97925mrna_121-409,defensingene,_complete_cds
s71824_2437-2881,_n-
cam=145_kda_neural_cell_adhesion_molecule_[human,_small_cell_lung_cancer_cell_li

- u05659_581-1049,17beta-hydroxysteroid_dehydrogenase_typemrna,_complete_cds
u06698_3269-3779,neuronal_kinesin_heavy_chain_mrna,_complete_cds_
u10485_1906-2326,lymphoid-restricted_membrane_protein_(jaw1)_mrna,_complete_cds
u11037_19-499,sel-1_like_mrna,_complete_cds
- 5 u11875_48-144,interleukin-
8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb4,_partial_cds/gb=u118
all_u12471_1014-1255,_thrombospondin-p50_gene_extracted_fromthrombospondin-
1_gene,_partial_cds
u16861_1076-1610,inward_rectifying_potassium_channel_mrna,_complete_cds
- 10 u28131_88-283,hmgi-c_chimeric_transcript_mrna,_partial_cds.
u29700cds_1308-1644:in_reversesequence,_8352-8382,anti-
mullerian_hormone_type_ii_receptor_precursor_
u35340_442-868,beta_b1-crystallin_mrna,_complete_cds_
u38227_3-411,testis-specific_hexokinase(hhkl1-tb)_mrna,_partial_cds/gb=u38227/_ntype=rna_
15 u45982cds_759-1035:in_reversesequence,_1110-1338,g_protein-coupled_receptor_gpr-9-
6_gene,_complete_c
u49742cds_744-984:in_reversesequence,_5287-5473,rhodopsin_gene,_complete_cds
u50146mrna_39-543,typeuropeptide_y_receptor_(npv_y2)_gene,_partial
u62433_2748-
- 20 3318,nicotinic_acetylcholine_receptor_alpha4_subunit_precursor,_mrna,_complete_cds_
u76366_4225-4720,treacher_collins_syndrome_(tcof1)_mrna,_complete_cds
u79303_939-1479,clone_23882_mrna,_complete_cds.
u83171_2313-2865,macrophage-derived_chemokine_precursor_(mdc)_mrna,_complete_cds_
x05323cds_426-792:not_in_gb_record,mrc_ox-2_gene_signal_sequence
- 25 x14830cds_1033-1423:in_reversesequence,_1547-
1571,mrna_for_muscle_acetylcholine_receptor_beta-subuni
x16666cds_422-841:in_reversesequence,_894-984,hox2i_mrna_from_the_hox2_locus
x64044cds_1066-1402:in_reversesequence,_1538-
1592,mmrna_for_large_subunit_of_splicing_factor_u2af_
30 x71135cds_1083-1308:in_reversesequence,_1752-1977,sox3_gene
x73113cds_2973-3339:in_reversesequence,_3430-3520,mrna_for_fast_mybp-c
all_x74496_1967-2520,mrna_for_prolyl_oligopeptidase
x76770mrna_1421-1931,pap_mrna
x78710mrna_2773-3247,mtf-1_mrna_for_metal-regulatory_transcription_factor
- 35 all_x79200_380-600,mrna_for_syt-
ssx,_synovial_sarcoma_translocation_junction/gb=x79200/_ntype=rna,mr
x83572_1392-1920,arsd_mrna_
all_x93921_942-1471,mrna_for_protein-tyrosine-phosphatase_(tissue_type:_testis)
y09321cds_1961-2375:in_reversesequence,_2423-2501,tafii105_mrna,_partial

- y09392exon#4_364-884,mrna_for_wsl-lr,_wsl-s1_and_wsl-s2_proteins_
y10141cds_56-286,dat1_gene,_partial,_vntr/gb=y10141_/ntype=dna_/annot=cds
z47038cds_267-698,partial_cdna_sequence,_clone_x101,_putative_microtubule-
associated;_protein_1a_(ma
- 5** z48510exon#5-7_47-6:in_reversesequence,_471,xg_mrna_(clone_fb1)/gb=z48510_/ntype=ma
z68274cds_182-
632,dna_sequence_from_cosmid_l129h7,_huntington_disease_region,_chromosome_4p16.3_cont
- Metagene 182
- 10** d16626_2478-3006,mrna_for_histidase,_complete_cds
d84424_1603-2053,fetal_brain_mrna_for_hyaluronan_synthase,_complete_cds
hg2999-ht4756_s_at_hg2999-ht4756_thyroid_peroxidase,_altsplice_2_
l31529cds_1308-1578:in_reversesequence,_1945-2053,beta1-
- 15** syntrophin_(snt_b1)_gene,_complete_cds_
m81650mrna_1200-1566,semenogelin_i_(semgi)_gene,_complete_cds_
u46023_4040-4544,xq28_mrna,_complete_cds_
all_z48570_1408-1991,sp17_gene_
- 20** Metagene 181
- af000545cds_461-
983,putative_purinergic_receptor_p2y10_gene,_complete_cds/gb=af000545_/ntype=dna_/an
d79995_4440-4806,mrna_for_kiaa0173_gene,_complete_cds
- 25** hg2314-ht2410_at_hg2314-ht2410_4-beta-galactosyltransferase
hg2325-ht2421_at_hg2325-ht2421_retinoic_acid_receptor,_gamma_2_
j00212mrna_393-761,leukocyte_interferon_(ifn-alpha)_alpha-f_mrna,_complete_cds_
l40394mrna_1312-1750,(clone_s194)_mrna,_3'_end_of_cds_
l77566mrna_1103-1655,dgs-i_mrna,_3'_end_
- 30** m15517cds#3_155-419:in_reversesequence,_803-
923,_ttr_gene_extracted_frommutant_prealbumin_gene_direct
m55267mrna_573-1035,evl2_protein_gene
m77235_7902-8418,cardiac_tetrodotoxin-insensitive_voltage-
dependent_sodium_channel_alpha_subunit_(hh
- 35** m80899_3582-4002,novel_protein_ahnak_mrna,_partial_sequence
all_m81780_3896-
4359,_smpd1_gene_(acid_sphingomyelinase)_extracted_fromacid_sphingomyelinase_(smpd1)
m86934_1529-1973,gs1_(protein_of_unknown_function)_mrna,_complete_cds
m90820_1286-1742,rapamycin-binding_protein_(fkbp25)_mrna,_complete_cds_

- s77415cds_660-948:in_reversesequence,_1449-1617,_melanocortin-
4_receptor_[human_genomic,_1671_nt]
u01212cds_153-411:in_reversesequence,_1715-
1943,olfactory_marker_protein_omp_gene,_complete_cds_
- 5** u03187_1505-2015,il12_receptor_component_mrna,_complete_cds
u09607_3463-3730,jak_family_protein_tyrosine_kinase_jak3_mrna,_complete_cds
u11717_3500-3743,calcium_activated_potassium_channel_hslo_mrna,_complete_cds_
u12779_1685-1959,map_kinase_activated_protein_kinase_mrna,_complete_cds_
all_u13061_518-1020,dehydroepiandrosterone_sulfotransferase_std_gene
- 10** u20325exon#3_57-
477,cocaine_and_amphetamine_regulated_transcript_cart_hcart_gene,_complete_cds_
u27330_1474-
1933,alpha_1,3_fucosyltransferase_fut5_mrna,_minor_transcript_ii,_complete_cds_
u30185_1981-2485,orphan_opioid_receptor_mrna,_complete_cds_
- 15** u32331_1974-2526,rig_mrna,_complete_sequence_
u46901mrna#1_1088-1640,nacp_gene_
u48437_1855-2293,amyloid_precursor-like_protein_mrna,_complete_cds_
u57057cds_1239-1515:in_reversesequence,_1871-2069,wd_protein_ir10_mrna,_complete_cds_
u63312exon#1_4-199:not_in_gb_record,cosmid_1112nc01-
- 20** 242e1_etv6_gene_exons_1b_andand_partial_cds/gb
u79266_972-1482,clone_23627_mrna,_complete_cds.
u79302_1414-1906,clone_23855_mrna,_partial_cds.
u80987_438-948,transcription_factor_tbx5_mrna,_complete_cds/gb=u80987/_ntype=ma_
u82759_406-571,homeodomain_protein_hoxa9_mrna,_complete_cds
- 25** all_x04201_619-1073,skeletal_muscle_1.3_kb_mrna_for_tropomyosin
x66364cds_454-814:in_reversesequence,_922,mrna_pssalre_for_serine/threonine_protein_kinase
all_x67734_4037-4470,mrna_for_transient_axonal_glycoprotein_tag-1
all_x69699_2155-2654,pax8_mrna_
all_x83378_4940-5523,mrna_for_putative_chloride_channel
- 30** Metagene 151
- ac002464cds_799-
1345,bac_clone_rg331p03,_complete_sequence/gb=ac002464/_ntype=dna/_annot=cds_
- 35** d87457_1568-2060,mrna_for_kiaa0281_gene,_complete_cds
hg4109-ht4379_at_hg4109-ht4379_olfactory_receptor_or17-30
u31215_3797-4037,metabotropic_glutamate_receptor_alpha_mglur1alpha_mrna,_complete_cds
x03473cds_270-552:in_reversesequence,_1054-1150,gene_for_histone_h1(0)

x06948cds_482-680:in_reversesequence,_918-1146,mrna_for_high_affinity_ige_receptor_alpha-subunit_(fc

all_z12173_1808-2361,gns_mrna_encoding_glucosamine-6-sulphatase

5 Metagene 124

all_x00038_599-718,h4_histone_gene_

Metagene 102

10

d25215_4320-4839,mrna_for_kiaa0032_gene,_complete_cds

d86974_5077-5308,mrna_for_kiaa0220_gene,_partial_cds_

hg3123-ht3299_at_hg3123-ht3299_homeotic_protein_gbx2_

l20861_3555-4089,proto-oncogene_(wnt-5a)_mrna,_complete_cds_

15 l29339mrna_1862-2324,na+/glucose_co-transporter_(sglt1)_gene

m91083mrna_989-1469,dna-binding_protein_(hrc1)_mrna,_complete_cds

m96684_609-867,pur_(pur-alpha)_mrna,_complete_cds

s90469_1802-2300,_cytochrome_p450_reductase_[human,_placenta,_mrna_partial,_2403_nt]

u05237_2192-2570,fetal_alz-50-reactive_clone(fac1)_mrna,_complete_cds_

20 u13896_2487-3015,homolog_of_drosophila_discs_large_protein,_isoform(hdlg-2)_mrna,_complete_cds

u47054_853-1357,putative_mono-adt-ribosyltransferase_(htmart)_mrna,_complete_cds_

u50327mrna_1463-2020,protein_kinase_c_substrate_80k-h_gene_(prkcsh)

u66615_4601-5165,swi/snf_complex_155_kda_subunit_(baf155)_mrna,_complete_cds_

25 u79288_1035-1509,clone_23682_mrna_sequence_

all_x69878_3909-4372,flt4_mrna_for_transmembrane_tyrosine_kinase_

all_x83618_1574-1995,mrna_for_3-hydroxy-3-methylglutaryl_coenzyme_a_synthase_

x96506cds_96-441:in_reversesequence,_600-631,mrna_for_nc2_alpha_subunit_

30 Metagene 90

m16653mrna_652-742,pancreatic_elastase_iib_mrna,_complete_cds

s83513_1328-1840,_pituitary_adenylate_cyclase_activating_polypeptide_[human,_mrna,_1940_nt]

u08049exon_19-475,peripheral_myelin_protein-22_(pmp22)_gene,_non-

35 coding_exon_1a/gb=u08049_/ntype=dna

u24056_1237-1787,inward_rectifier_k+_channel_protein_(hirk2)_mrna,_complete_cds

u43885_1914-2442,grb2-associated_binder-1_mrna,_complete_cds_

z49105mrna_1064-1259,hd21_mrna_

Metagene 56

- ab000467_1590-2118, clone_res4-25, partial_cds
d16181exon_1310-1712, pmp2_gene_for_peripheral_myelin_protein_2_
- 5 hg4165-ht4435_at_hg4165-ht4435_hpc-1_
117328_1400-1868, pre-t/nk_cell_associated_protein_(3cl)_mrna, complete_cds_
122650_84-636, early_lymphoid_activation_protein_(epag)_mrna_sequence_
m24902mrna_2694-3018, prostatic_acid_phosphatase_mrna, complete_cds_
m82882_3023-3503, cis-acting_sequence_
- 10 s76617_2203-2569, blk=protein_tyrosine_kinase_[human, b_lymphocytes, mrna, 2608_nt]_
s78467_987-1384, pig-a-
ii=glycoinositol_phospholipid_anchor_synthetic_element_[human, paroxysmal_noc
u20350_2697-3045, g_protein-coupled_receptor_v28_mrna, complete_cds_
u46194_1466-1997, renal_cell_carcinoma_antigen_rage-4_mrna, complete_putative_cds_
- 15 u66726_2378-
2846, testis_specific_rna_binding_protein_(spgyla)_mrna, complete_cds, testis_specific_rna
u85265_7-
63, down_syndrome_critical_region(dscr1)_gene, alternative_exon/gb=u85265_/ntype=rna_

20 Metagene 35

- af012024_658-1175, integrin_cytoplasmic_domain_associated_protein_(icap-
1b)_mrna, complete_cds/gb=af0
d23660_889-1369, mrna_for_ribosomal_protein, complete_cds_
- 25 d31883_6153-6711, mrna_for_kiaa0059_gene, complete_cds
d78361_504-942, mrna_for_ornithine_decarboxylase_antizyme, orfand_orf_2
d86331_1281-1777, mt2-mmp_gene_for_matrix_metalloprotein, complete_cds
hg1103-ht1103_at_hg1103-ht1103_guanine_nucleotide-binding_protein_ral, ras-oncogene_related
hg180-ht180_at_hg180-ht180_ahnak-a_nucleoprotein_ahnak-a_
- 30 hg2873-ht3017_at_hg2873-ht3017_ribosomal_protein_l30_homolog_
hg3362-ht3539_s_at_hg3362-ht3539_chromosomal-translocation_associated_gene_ltg19/enl_
hg3395-ht3573_s_at_hg3395-ht3573_dnaj_homolog, altsplice_form_2
hg3549-ht3751_at_hg3549-ht3751_wilm_tumor-related_protein
hg4319-ht4589_at_hg4319-ht4589_ribosomal_protein_l5
- 35 hg821-ht821_at_hg821-ht821_ribosomal_protein_s13_
j03592_707-1085, adp/atp_translocase_mrna, 3'_end, clone_phat8
j04617cds_1069-1364:in_reversesequence, 3823-4030, elongation_factor_ef-1-
alpha_gene, complete_cds_
104483_39-272, ribosomal_protein_s21_(rps21)_mrna, complete_cds_

- 106499mrna_4-301,ribosomal_protein_l37a_(rpl37a)_mrna,_complete_cds_
 106505mrna_259-553,ribosomal_protein_l12_mrna,_complete_cds
 107868_4919-5429,receptor_tyrosine_kinase_(erbb4)_gene,_complete_cds
 111566_77-521,ribosomal_protein_l18_(rpl18)_mrna,_complete_cds
- 5** all_m10277_3236-3578,cytoplasmic_beta-actin_gene,_complete_cds_
 m17886mrna_7-475,acidic_ribosomal_phosphoprotein_p1_mrna,_complete_cds_
 m18000cds_78-360,ribosomal_protein_s17_gene,_complete_cds
 m19828exon#8_1305-1576:in_reversesequence,_14367-14518,apolipoprotein_b-100_(apob)_gene_
 m24194mrna_504-
- 10** 1023,mhc_protein_homologous_to_chicken_b_complex_protein_mrna,_complete_cds_
 all_m31520_25-
 590,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna_
 m31520mrna_2-
 106,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna_
 m36072_368-770,ribosomal_protein_l7a_(surf_3)_large_subunit_mrna,_complete_cds_
15 m55409_556-1069,pancreatic_tumor-related_protein_mrna,_3'_end
 m58603_3120-3600,nuclear_factor_kappa-b_dna_binding_subunit_(nf-kappa-
 b)_mrna,_complete_cds
 m60854_19-373,ribosomal_protein_s16_mrna,_complete_cds_
20 m64098_3873-4305,high_density_lipoprotein_binding_protein_(hbp)_mrna,_complete_cds_
 m64716mrna_31-451,ribosomal_protein_s25_mrna,_complete_cds_
 m81757_49-421,s19_ribosomal_protein_mrna,_complete_cds_
 s79522_19-481,_ubiquitin_carboxyl_extension_protein_[human,_mrna,_540_nt]_
 u07804_1857-2384,dna_topoisomerase_i_mrna,_partial_cds_
25 u07806_2865-3382,camptothecin_resistant_clone_cem/c2_dna_topoisomerase_i_mrna,_partial_cds_
 u09953_153-621,ribosomal_protein_l9_mrna,_complete_cds_
 u14968_133-451,ribosomal_protein_l27a_mrna,_complete_cds_
 u14969_43-451,ribosomal_protein_l28_mrna,_complete_cds_
 u14971_91-661,ribosomal_protein_s9_mrna,_complete_cds_
30 u14973_13-235,ribosomal_protein_s29_mrna,_complete_cds_
 u25789_19-481,ribosomal_protein_l21_mrna,_complete_cds_
 u49352_548-1106,liver_2,4-dienoyl-coa_reductase_mrna,_complete_cds_
 u49785_311-641,d-dopachrome_tautomerase_mrna,_complete_cds.
 u78027mrna#3_3-350,_1441_gene_(l44-
35 like_ribosomal_protein)_extracted_frombruton_tyrosine_kinase_(btk
 u79273_851-1127,clone_23933_mrna_sequence
 u83461_1235-
 1619,putative_copper_uptake_protein_(hctr2)_mrna,_complete_cds/gb=u83461/_ntype=rna

- x01677cds_629-983:in_reversesequence,_1109-1229,liver_mrna_for_glyceraldehyde-3-phosphate_dehydrogen
- x03342cds_51-375:in_reversesequence,_439-445,mrna_for_ribosomal_protein_l32_
- x06617mrna_31-475,mrna_for_ribosomal_protein_s11_
- 5** x16064cds_147-483:in_reversesequence,_625-745,mrna_for_translationally_controlled_tumor_protein_
- x17206cds_111-585:in_reversesequence,_885,mrna_for_llrep3_
- x52966cds_11-299:in_reversesequence,_19-373,mrna_for_ribosomal_protein_l35a_
- x55715cds_228-618:in_reversesequence,_748-784,hums3_mrna_for_40s_ribosomal_protein_s3_
- 10** x56932cds_114-576:in_reversesequence,_611-623,mrna_for_23_kd_highly_basic_protein_
- x56997mrna#1_19-475:not_in_gb_record,uba52_gene_coding_for_ubiquitin-52_amino_acid_fusion_protein
- all_x64707_401-888,bbc1_mrna_
- x67247mrna_116-662,rps8_gene_for_ribosomal_protein_s8_
- 15** x69150mrna_25-403,_l06432mrna_for_ribosomal_protein_s18
- x79234cds_115-511,mrna_for_ribosomal_protein_l11_
- z26876_43-328,gene_for_ribosomal_protein_l38_
- z28407cds_220-703:in_reversesequence,_809-818,mrna_for_ribosomal_protein_l8_
- z49148cds_2-418:in_reversesequence,_18-589,mrna_for_ribosomal_protein_l29_
- 20** z69043cds_66-489:in_reversesequence,_30-598,mrna_translocon-associated_protein_delta_subunit_precurs
- all_z70759_4-251,mitochondrial_16s_rna_gene_(partial).
- Metagene 2
- 25** d13633_2141-2597,mrna_for_kiaa0008_gene,_complete_cds
- l19783_895-1351,gpi-h_mrna,_complete_cds_
- l33262_1751-2273,dna_repair_and_recombination_homologue_(rad52)_gene,_complete_cds
- m29927exon_229-703,ornithine_aminotransferase_gene_
- 30** u09087_2090-2543,thymopoietin_beta_mrna,_complete_cds
- u67611_788-
- l130:not_in_gb_record,_mouse_transaldolase_gene_mrna,_complete_cds/gb=u67611/_ntype=ma_
- u72936_9836-
- l0377,putative_dna_dependent_atpase_and_helicase_(atrx)_mrna,_alternatively_spliced_prod
- 35** all_x67491_839-1137,gene_for_glutamate_dehydrogenase_
- x99586cds_12-223:in_reversesequence,_329,mrna_for_smt3c_protein_
- z46629mrna_3352-3730,sox9_mrna

Metagene 1

- 100137cds#1_6-234:in_reversesequence,_8-
 134:not_in_gb_record_ghrf_gene_(growth_hormone_releasing_fa
 m33478mrna_653-1049,33-kda_phototransducing_protein_mrna,_complete_cds_
- 5 all_m34344_114-364:in_m34344cds_3032-3069,platelet_glycoprotein_iib_(gpiib)_gene
 m62810_1350-1818,mitochondrial_transcription_factormrna,_complete_cds_
 m73239mrna_2114-2638,(clone_sf1)_hepatocyte_growth_factor_(hgf)_mrna,_complete_cds_
 m81758_7258-7798,skeletal_muscle_voltage-
 dependent_sodium_channel_alpha_subunit_(skm1)_mrna,_complet
- 10 all_u51561_10617-28244:in_u51561cds_50,cosmid_n79e2,_complete_sequence
 u75309_1813-2376,tbp-associated_factor_(htafii100)_mrna,_partial_cds_
 u95090mrna_2166-2418:in_fullsequence,_36716-
 36854,chromosomecosmid_f19541,_complete_sequence
 all_x13766_14-551,beta-casein_mrna_3'-terminal_fragment_
- 15 Metagene 434
- all_m26665_267-307,histatin(his2)_mrna,_complete_cds,histatin(his2)_mrna,_complete_cds
 m28130mrna_654-1002,interleukin(il8)_gene,_complete_cds
- 20 m33684cds_288-788,(clone_lambda-10-2)_non-receptor_tyrosine_phosphatase(ptpn1)_gene_
 u10492_1894-2266,mox1_protein_(mox1)_mrna,_complete_cds
 u18985_2460-2922,triadin_mrna,_complete_cds
 u48213mrna_1031-1601,d-site_binding_protein_gene,_promoter_region_and
- 25 Metagene 408
- d42039_3568-4074,mrna_for_kiaa0081_gene,_partial_cds_
 d55643_443-1019,spleen_pabl_(pseudoautosomal_boundary-
 like_sequence)_mrna,_clone_sp2/gb=d55643/_ntyp
- 30 hg3993-ht4263_at_hg3993-ht4263_cpg-enriched_dna,_clone_sl2_
 102785_2412-2790,colon_mucosa-associated_(dra)_mrna,_complete_cds_
 m28826_976-1252,thymocyte_antigen_cd1b_mrna,_complete_cds
- 35 Metagene 211
- ab006190_705-1179,mrna_for_aquaporin_6,_complete_cds/gb=ab006190/_ntype=rna_
 d13642_4248-4722,mrna_for_kiaa0017_gene,_complete_cds
 d31815_797-1295,mrna_for_smp-30_(senescence_marker_protein-30),_complete_cds_

- d31846exon#4_179-713, gene_for_aquaporin-2_water_channel_exon1-4_complete_cds_
d38305_701-1181, mrna_for_tob_complete_cds_
d63482_1722-2226, mrna_for_kiaa0148_gene_complete_cds
d82070_285-843, ac1_mrna_complete_cds
- 5** d85527_37-349, mrna_for_lim_domain_partial_cds/gb=d85527/_ntype=rna
d87460_2023-2503, mrna_for_kiaa0270_gene_partial_cds_
d87468_2496-2886, mrna_for_kiaa0278_gene_partial_cds_
hg1649-ht1652_at_hg1649-ht1652_elastase_
hg1800-ht1823_at_hg1800-ht1823_ribosomal_protein_s20_
- 10** hg2261-ht2352_at_hg2261-ht2352_antigen_prostate_specific_altsplice_form_3
hg2604-ht2700_at_hg2604-ht2700_pan-2_
hg3432-ht3618_at_hg3432-ht3618_fibroblast_growth_factor_receptor_k-sam_altsplice_1
hg3987-ht4257_at_hg3987-ht4257_cpg-enriched_dna_clone_e06_
hg4036-ht4306_at_hg4036-ht4306_retinoblastoma_
- 15** hg4051-ht4321_at_hg4051-ht4321_choline_acetyltransferase_
hg4662-ht5075_at_hg4662-
ht5075_omega_light_chain_immunoglobulin_lambda_light_chain_related
hg896-ht896_at_hg896-ht896_thrombospondin_
hg919-ht919_at_hg919-ht919_dna_polymerase_epsilon_catalytic_subunit
- 20** all_k03460_3-379, alpha-tubulin_isotype_h2-alpha_gene_last_exon
l20965_3164-3680, phosphodiesterase_mrna_complete_cds
l23852mrna_1122-1674,(clone_z146)_retinal_mrna_3'_end_and_repeat_region
l36720_661-1219, bystin_mrna_complete_cds_
l42621mrna_1775-2231, ly-9_mrna_complete_cds
- 25** l77561mrna_583-1093, dgs-d_mrna_3'_end
all_m13903_1676-2031, involucrin_mrna_
m27749_245-323, immunoglobulin-related_14.1_protein_mrna_complete_cds, immunoglobulin-related_14.1_pr
m30185mrna_1234-1666, cholesteryl_ester_transfer_protein_mrna_complete_cds_
- 30** m34079_830-1298, immunodeficiency_virus_tat_transactivator_binding_protein-1_(tbp-1)_mrna_complete_c
m34182mrna#1_1112-1517, testis-specific_protein_kinase_gamma-subunit_mrna_complete_cds_
s76992_2182-2710, vav2=vav_oncogene_homolog_[human_fetal_brain_mrna_partial_2753_nt]_
s78771_1149-1661, nat=cpg_island-associated_gene_[human_mrna_1741_nt]_
s81003_130-640, l-
- 35** ubc=ubiquitin_conjugating_enzyme_[human_odontogenic_keratocysts_mrna_partial_68
u01157_2506-2992, glucagon-like_peptide-
l_receptor_mrna_with_ca_dinucleotide_repeat_complete_cds_
u01922_405-921, btk_region_clone_fci-12_mrna

- u08336_368-872,basic_helix-loop-helix_transcription_factor_mrna,_complete_cds
u09210_1910-2396,vesicular_acetylcholine_transporter_mrna,_complete_cds
u20908cds_13-193,clone_350/2_melanoma_ubiquitous_mutated_protein_(mum-
1)_gene,_partial_cds/gb=u20908
- 5 u31903_2052-2510,creb-rp_(creb-rp)_mrna,_complete_cds
u34880_1699-2179,dph2l_mrna,_complete_cds
u37673_2848-3412,neuron-
specific_vesicle_coat_protein_and_cerebellar_degeneration_antigen_(beta-nap)
u39576_2486-2852,butyrophilin_precursor_mrna,_complete_cds_
- 10 u49089_2571-3075,neuroendocrine-dlg_(ne-dlg)_mrna,_complete_cds
u52696_703-742,adrenal_creb-rp_homolog_(creb-rp),_complete_cds,_and_tenascin-
x_(xb),_partial_cds,_mr
u59302_4047-4617,steroid_receptor_coactivator-1_f-src-1_mrna,_complete_cds_
u62317mrna#3_1056-
- 15 1488,_hypothetical_protein_384d8gene_extracted_from_chromosome_22q13_bac_clone_cit
u66059cds#21_49-283:in_reversesequence,_207121-207343,germline_t-
cell_receptor_beta_chain_dopamine-b
u73328_918-1314,dlx7_(dlx7)_mrna,_complete_cds_
u76764_2544-3054,cd97_mrna,_complete_cds_
- 20 u78521_655-1111,immunophilin_homolog_ara9_mrna,_complete_cds
u78678_191-683,thioredoxin_mrna,_nuclear_gene_encoding_mitochondrial_protein,_complete_cds_
u79258_861-1407,clone_23732_mrna,_partial_cds
u81001_2773-3039,snrpn_mrna,_3' utr,_partial_sequence
u90543_2445-
- 25 2739,butyrophilin_(btfl)_mrna,_complete_cds,butyrophilin_(btfl)_mrna,_complete_cds
u96629mrna#2_3194-
3722,_2a8.2_gene_(unknown_protein_cit987sk_2a8_1)_extracted_fromchromosomebac_clon
all_x14085_1251-1422,mrna_for_beta-1,4-galactosyltransferase_(ec_2.4.1.22)_
all_x62573_1608-2161,rna_for_fc_receptor,_tc9
- 30 all_x66785_2930-3511,mrna_for_transacylase_(dbt)_
all_x78817_2647-3236,partial_c1_mrna_
all_x83368_4789-5345,mrna_for_phosphatidylinositolkinase_gamma
x96401_1673-2186,mrna_for_rox_protein
x96924mrna_1184-1215,gene_encoding_mitochondrial_citrate_transport_protein
- 35 all_x99133_5342-5685:in_x99133cds_563-597:not_in_gb_record,ngal_gene_
z31560cds_475-923:in_reversesequence,_953,sox-2_mrna_(partial)

Metagene 145

- ab000450_1298-1730,mrna_for_vrk2,_complete_cds_
 ab000464_3281-3743,_clone_res4-24a,_exon_1,_2,_3,_4_
 ab001106_3542-4088,mrna_for_glia_maturation_factor,_complete_cds_
 d00723_642-
- 5** 1110,mrna_for_hydrogen_carrier_protein,_a_component_of_an_enzyme_complex,_glycine_synthas
 d11151exon_1936-2434,dna_for_endothelin-a_receptor,_5'_flanking_region_and_
 d12625_2036-2219,mrna_for_nfl_protein_isoform_(neurofibromin_isoform),_complete_cds
 d12676_1884-2220,mrna_for_lysosomal_sialoglycoprotein,_complete_cds
 d13635_4583-5117,mrna_for_kiaa0010_gene,_complete_cds
- 10** d13789_1594-2062,mrna_for_n-acetylglucosaminyltransferase_iii,_complete_cds
 d14662_1082-1592,mrna_for_kiaa0106_gene,_complete_cds
 d21163_3183-3693,mrna_for_kiaa0031_gene,_complete_cds
 d86549_609-969,mrna_for_p97_homologous_protein,_partial_cds
 d88532_3016-3328,mrna_for_p55pik,_complete_cds_
- 15** l04733_1785-2265,kinesin_light_chain_mrna,_complete_cds_
 l08488_1206-1644,inositol_polyphosphate_1-phosphatase_mrna,_complete_cds_
 l13434_2304-2850,chromosome_3p21.1_gene_sequence,_complete_cds_
 l22009_1642-2056,hnmp_h_mrna,_complete_cds
 l27476_3901-4429,x104_mrna,_complete_cds_
- 20** l38933mrna_883-
 l393,_the_longest_open_reading_frame_predicts_a_protein_of_202_amino_acids,_with_fair
 l41939mrna_3197-3731,(clone_fbk_iii_11c)_protein-tyrosine_kinase_(drt)_mrna,_complete_cds_
 m37190mrna_1220-1796,ras_inhibitor_mrna,_3'_end
 all_m54968_5180-5775,k-ras_oncogene_protein_mrna,_complete_cds_
- 25** m64936_2808-3264,retinoic_acid-inducible_endogenous_retroviral_dna
 m91029exon#3_2581-2977,amp_deaminase_(ampd2)_mrna_
 s59049_786-1314,_bl34=b_cell_activation_gene_[human,_mrna,_1398_nt]
 s73149mrna_293-827,_insulin-
 like_growth_factor_ii_{intron_7}_[human,_genomic,_1702_nt]/gb=s73149_/nt
- 30** u08023_3037-3529,cellular_proto-oncogene_(c-mer)_mrna,_complete_cds
 u08316_1719-2235,insulin-stimulated_protein_kinase(ispk-1)_mrna,_complete_cds_
 u15782_2237-2681,cleavage_stimulation_factor_77kda_subunit_mrna,_complete_cds
 u23028_1702-2236,eukaryotic_initiation_factor_2b-epsilon_mrna,_partial_cds_
 u39487_3877-4339,xanthine_dehydrogenase/oxidase_mrna,_complete_cds_
- 35** u85658_2310-2736,transcription_factor_erf-1_mrna,_complete_cds_
 x62083_3969-4029,mrna_for_drosophila_female_sterile_homeotic_(fsh)_homologue_
 all_x69962_4188-4308,fnr-1_mrna
 all_x82125_2007-2368,hok-2_mrna_for_zinc_finger_protein

Metagene 143

- d14663_785-1259,mrna_for_kiaa0107_gene,_complete_cds_
d38496_3615-4170,mrna_for_lztr-1,_complete_cds_
5 d42084_2112-2610,mrna_for_kiaa0094_gene,_partial_cds_
d49400_115-655,fetus_brain_mrna_for_vacuolar_atpase,_complete_cds
d84294mrna_8552-9020,mrna_for_tprdi,_complete_cds
d86988_4716-5220,mrna_for_kiaa0221_gene,_complete_cds
d87445_6334-6892,mrna_for_kiaa0256_gene,_complete_cds
10 hg1322-ht5143_s_at_hg1322-ht5143_small_nuclear_ribonucleoprotein,_polypeptide_altsplice_2_
hg3484-ht3678_s_at_hg3484-ht3678_protein_kinase
j04794mrna_567-1071,aldehyde_reductase_mrna,_complete_cds
l09209_3114-3666,amyloid_protein_homologue_mrna,_complete_cds_
l35249mrna_2225-2690,vacuolar_h+-atpase_mr_56,000_subunit_(ho57)_mrna,_complete_cds_
15 l49380mrna_2916-3414,clone_b4_transcription_factor_zfm1_mrna,_complete_cds
m14483mrna_41-443_ptma_gene_extracted_fromprothymosin_alpha_mrna,_complete_cds_
m26708_549-1008,prothymosin_alpha_mrna_(prot-alpha),_complete_cds
m91432mrna_1664-2144,medium-chain_acyl-coa_dehydrogenase_(mcd)_gene_
u00115_3001-3451,zinc-finger_protein_(bcl-6)_mrna,_complete_cds
20 u09825_3156-3522,acid_finger_protein_mrna,_complete_cds
u22970mrna#1_205-749,_16-jun_gene_(interferon-inducible_peptide_precursor)_extracted_frominterferon-
u26424_2237-2735,ste20-like_kinase_(mst2)_mrna,_complete_cds_
u45328_591-1079,ubiquitin-conjugating_enzyme_(ube2i)_mrna,_complete_cds
25 u60061_905-1325,fez2_mrna,_partial_cds_
u61397_875-1173,ubiquitin-homology_domain_protein_pic1_mrna,_complete_cds
u80017mrna#3_892-
1444,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcriptio
u91930_4196-4682,ap-3_complex_delta_subunit_mrna,_complete_cds_
30 u91931_3081-3489,ap-3_complex_beta3a_subunit_mrna,_complete_cds
u91932_778-1210,ap-3_complex_sigma3a_subunit_mrna,_complete_cds
u92014_817-1366,clone_121711_defective_mariner_transposon_hsmar2_mrna_sequence_
all_x03484_2418-2947,mrna_for_raf_oncogene_
x60787mrna_2434-3000,mrna_for_transcription_factor_ilf_
35 all_x62534_726-1137,hmg-2_mrna_
all_x63692_4825-5348,mrna_for_dna_(cytosin-5)-methyltransferase
x65784cds_58-399,car_gene
all_x66899_1902-2323,ews_mrna
x69838cds_2756-2924;in_reversesequence,_3043-3331,mrna_for_g9a

- all_x69910_2339-2892,p63_mrna_for_transmembrane_protein
 all_x70394_2591-3156,ozf_mrna
 all_x72889_5441-5844,hbrm_mrna_
 all_x73478_2042-2637,hptpa_mrna
5 all_x79536_1005-1156,mrna_for_hnmpcore_protein_a1.
 all_x86691_5882-6399,mrna_for_218kd_mi-2_protein_
 all_x89750_1061-1512,mrna_for_tgif_protein_
 all_x95404_482-1047,mrna_for_non-muscle_type_cofilin_
 x95735_1628-2168,mrna_for_zyxin_2
10 all_x98743_2619-3112,mrna_for_rna_helicase_(myc-regulated_dead_box_protein)
 all_y00815_7107-7684,mrna_for_lca-homologlar_protein_(leukocyte_antigen_related)_
 all_y08614_3715-4118,mrna_for_crm1_protein_
 all_z24724_1263-1840,polya_site_dna
 z26491exon#5_388-430,gene_for_catechol_o-methyltransferase_
15 all_z29505_1140-1468,mrna_for_nucleic_acid_binding_protein_sub2.3

Metagene 108

- ab003102_956-1442,mrna_for_proteasome_subunit_p44.5,_complete_cds
20 d14659_648-1134,mrna_for_kiaa0103_gene,_complete_cds_
 d21260_5600-6002,mrna_for_kiaa0034_gene,_complete_cds
 d31885_1773-2169,mrna_for_kiaa0069_gene,_partial_cds_
 d38551_3082-3592,mrna_for_kiaa0078_gene,_complete_cds
 d38555_3911-4421,mrna_for_kiaa0079_gene,_complete_cds
25 d64142mrna_625-1177,mrna_for_histone_h1x,_complete_cds_
 d78129_568-
 1024,adult_(34_year_old)_male_liver_mrna_for_squalene_epoxidase,_partial_cds/gb=d78129_/n
 d85429exon#3_813-1347,dna_for_heat_shock_protein_40,_complete_cds
 d86972_4190-4610,mrna_for_kiaa0218_gene,_complete_cds
30 d87120_1936-2314,cancellous_bone_osteoblast_mrna_for_gs3786,_complete_cds
 hg2788-ht2896_at_hg2788-ht2896_calcyclin_
 hg2874-ht3018_at_hg2874-ht3018_ribosomal_protein_l39_homolog_
 l09604_339-819,differentiation-dependent_a4_protein_mrna,_complete_cds
 l19779_7-496,histone_h2a.2_mrna,_complete_cds_
35 l38928mrna_274-832,5,10-methenyltetrahydrofolate_synthetase_mrna,_complete_cds
 l42542mrna_3353-3803,rlip76_protein_mrna,_complete_cds_
 m31642mrna_802-1288,hypoxanthine_phosphoribosyltransferase_(hprt)_mrna,_complete_cds_
 m58460_1311-1490,75-kd_autoantigen_(pm-scl)_mrna,_complete_cds_
 all_m59830_2432-2661,mhc_iii_hsp70-2_gene_(hla),_complete_cds

- m60922_1971-2427,surface_antigen_mrna,_complete_cds
 all_m90516_2559-3058,glutamine:fructose-6-phosphate_amidotransferase_(gfat)_mrna,_complete_cds_
 u76992_2137-2533,tat-sf1_mrna,_complete_cds
- 5** x55079mrna_3257-3366:not_in_gb_record,_gaa_gene_extracted_fromlysosomal_alpha-glucosidase_gene_exon_
 x57985mrna#1_1652-
 2168,_gl105_gene_(histone_h2b)_extracted_fromgenes_for_histones_h2b.1_and_h2a_
 y07867cds_643-787:in_reversesequence,_1087-1237,mrna_for_pirin,_isolate_1_
- 10** Metagene 50
- d10667_2830-3307,mrna_for_smooth_muscle_myosin_heavy_chain_
 m72885mrna_207-750,_g0s2_gene_extracted_fromgos2_gene,_5'_flank_and_cds_
15 all_u22028_8029-
 8330,cytochrome_p450_(cyp2a13)_gene,_complete_cds,cytochrome_p450_(cyp2a13)_gene,_co
 u92459_2702-3194,metabotropic_glutamate_receptormrna,_complete_cds
- Metagene 18
- 20** u39231_1739-1979,gip_receptor_(gipr)_mrna,_complete_cds
 all_v00503_2330-2452,mrna_encoding_pro-alpha-2_chain_of_type_i_procollagen(major_part)_
 all_x79200_380-600,mrna_for_syt-
 ssx,_synovial_sarcoma_translocation_junction/gb=x79200_/ntype=rna,mr
- 25** Metagene 13
- all_d32001_61-294,husaalg_gene_for_serum_amyloid_a1_gamma,_exonand_intron_3_
 hg2059-ht2114_at_hg2059-ht2114_arrestin,_beta_2
30 hg2480-ht2576_at_hg2480-ht2576_fm1p-related_receptor_i_
 hg2809-ht2920_s_at_hg2809-ht2920_lung_surfactant_protein_d_
 hg3107-ht3283_s_at_hg3107-ht3283_plasma_membrane_calcium_pump_hpmca2a
 hg759-ht759_s_at_hg759-ht759_adrenergic_receptor,_beta_1_
 j05036mrna_1546-2119,cathepsin_e_mrna,_complete_cds
35 j05073cds_239-641,phosphoglycerate_mutase_(pgam-m)_gene,_complete_cds
 k02766_2028-2436,complement_component_c9_mrna,_complete_cds
 l29008_2014-2464,l-iditol-2_dehydrogenase_mrna,_complete_cds_
 l33477_3692-4142,(clone_8b1)_br-cadherin_mrna,_complete_cds
 l35592mrna#1_1633-2107,germline_mrna_sequence_

- 137112mrna_1710-1816,vasopressin_v3_receptor_mrna_complete_cds_
 140933cds_1218-1470:in_reversesequence,_1639-1819,phosphoglucomutase-
 related_protein_(pgmrp)_gene,_c
 all_m80333_1628-2079,m5_muscarinic_acetylcholine_receptor_gene_complete_cds_
- 5** m85217_2529-2955,k+_channel_protein_(hkl3)_mrna_complete_cds
 m89473_1394-1706,neurokininreceptor_(nk3r)_mrna_complete_cds_
 m96859_3150-3630,dipeptidyl_aminopeptidase_like_protein_mrna_complete_cds_
 u09609_2198-2708,p80ht_(p80ht/nkfb-2)_mrna_complete_cds_
 u13737_2046-2556,cysteine_protease_cpp32_isoform_alpha_mrna_complete_cds_
- 10** u14910_910-1360,rpe-retinal_g_protein-coupled_receptor_(rgr)_mrna_complete_cds
 u18671mrna_2702-3266,stat2_gene_complete_cds_
 u29615_1098-1530,chitotriosidase_precursor_mrna_complete_cds
 u31929cds_1063-1361:in_reversesequence,_6372-
 6576,orphan_nuclear_receptor_(dax1)_gene_complete_cds_
- 15** u63336_1666-2062,mhc_i_region_proline_rich_protein_mrna_complete_cds
 u65404_1140-1530,erythroid-specific_transcription_factor_eklf_mrna_complete_cds.
 u78180_3340-3880,sodium_channel(hbnac2)_mrna_alternatively_spliced_complete_cds_
 u85992_1236-1596,clone_image:35527_unknown_protein_mrna_partial_cds_
 all_u87408_1441-1952,clone_image:74593_unknown_protein_mrna_partial_cds_
- 20** v00535mrna#1_253-692,_interferon_betagene_extracted_from_gene_forfibroblast_interferon_beta_1
 all_x04729_2-263,mrna_for_plasminogen_activator_inhibitor_typen-
 terminus/gb=x04729/_ntype=rna_
 x54816_at_x54816_x54816,not_in_gb_record,gene_for_alpha-1-microglobulin-bikunin_exons_5-
 jan_(encodi
- 25** all_x54938_1175-1752,mrna_for_inositol_1,4,5-triphosphate_3-kinase_
 x55889cds_264-546:not_in_gb_record,gene_for_ciliary_neurotrophic_factor_exon_1_
 x55990mrna_163-489,ecp_gene_for_eosinophil_cationic_protein_
 all_x66141_261-784,mrna_for_cardiac_ventricular_myosin_light_chain-2_
 x97748mrna_59-189,ptx3_gene_promotor_region/gb=x97748/_ntype=dna/_annot=mrna_
- 30** all_x99140_1407-1822,mrna_for_hair_keratin_hhb5_
 y10376cds_888-1158:in_reversesequence,_1222-1408,mrna_for_sirp-beta1_
 y13115cds_2477-2879:in_reversesequence,_3061,mrna_for_serine/threonine_protein_kinase_sak
 z24680mrna_3558-4044,garp_gene_mrna_complete_cds
 all_z31357_967-1502,mrna_for_cysteine_dioxygenase_type_1_
- 35** Metagene 486

 all_m60751_910-1163,histone_h2b.1_(h2b)_gene_complete_cds_
 x81333cds_1730-2078:in_reversesequence,_2130-2220,mrna_for_pph_beta_subunit_protein_

all_y00317_1618-2081,mrna_for_liver_microsomal_udp-glucuronosyltransferase_(udpgt)_

Metagene 397

- 5 u91618_167-671,proneurotensin/proneuromedin_n_mrna,_complete_cds.
x78121mrna_1730-1940:in_reversesequence,_1970-2036,mrna_for_choroideremia_
y07828cds_345-675:in_reversesequence,_844-994,mrna_for_ring_protein_

Metagene 373

10

d26350_10043-10481,mrna_for_typeinositol_1,4,5-trisphosphate_receptor,_complete_cds_
hg4747-ht5195_at_hg4747-ht5195_nadh-ubiquinone_oxidoreductase,_51_kda_subunit
m22612_188-759,pancreatic_trypsin(try1)_mrna,_complete_cds
all_x74008_1842-2245,mrna_for_protein_phosphatasegamma

15

Metagene 356

- d26156_4588-5166,mrna_for_transcriptional_activator_hsnf2b,_complete_cds_
d86964_5449-5995,mrna_for_kiaa0209_gene,_partial_cds_
20 hg3141-ht3317_f_at_hg3141-ht3317_nadh-ubiquinone_oxidoreductase,_39_kda_subunit
k03494cds_557-1062:in_reversesequence,_115,green_cone_photoreceptor_pigment_gene_1
119437_857-1211,transaldolase_mrna_containing_transposable_element,_complete_cds_
l24783_78-624,mrna_fragment/gb=l24783_/ntype=rna
l28010_1292-1748,hnrnp_f_protein_mrna,_complete_cds_
25 m80254_492-840,cyclophilin_isoform_(hcyp3)_mrna,_complete_cds
m88108_2156-2636,p62_mrna,_complete_cds
u19251_s_at_u19251_u19251,not_in_gb_record,neuronal_apoptosis_inhibitory_protein_mrna,_comp
lete_cds
u24166_2107-2395,eb1_mrna,_complete_cds
30 u33936_578-1050,adenosine_kinase_mrna,_complete_cds/gb=u33936_/ntype=rna_
u51990_867-1269,hprp18_mrna,_complete_cds
u60521_1398-1860,protease_promch6_(mch6)_mrna,_complete_cds
u62389_31-409,putative_cytosolic_nadp-
dependent_isocitrate_dehydrogenase_mrna,_partial_cds/gb=u62389
35 u72511_440-596,b-cell_receptor_associated_protein_(hbap)_mrna,_partial_cds_
x05196exon#9_2-458:in_reversesequence,_3199:not_in_gb_record,aldolase_c_gene_
all_x12953_859-1130,rab2_mrna,_ypt1-related_and_member_of_ras_family_
all_x17644_1976-2559,gstl-hs_mrna_for_gtp-binding_protein
x57152mrna#1_536-962,gene_for_casein_kinase_ii_subunit_beta_(ec_2.7.1.37)_

- x78338mrna_5278-5824,synthetic_adenovirus_transformedretina_cell_line_mrp_mrna_
all_x91247_3261-3700,mrna_for_thioredoxin_reductase
x97065cds_1852-2260:in_reversesequence,_2389-2395,mrna_for_sec23b_isoform,_2450bp_
x98411cds_2016-2256:in_reversesequence,_2340-2490,mrna_for_myosin-ie
- 5 x99209_1549-2053,mrna_for_arginine_methyltransferase_
all_z11695_2189-2736,40_kda_protein_kinase_related_to_rat_erk2_
z29481cds_624-792:in_reversesequence,_898-1186,mrna_for_3-
hydroxyanthranilic_acid_dioxygenase
- 10 Metagene 154
- d00408_1373-1921,fetal_liver_cytochrome_p-450_(p-
450_hfla),_complete_cds,fetal_liver_cytochrome_p-45
d13638_5003-5557,mrna_for_kiaa0013_gene,_complete_cds
- 15 hg2320-ht2416_at_hg2320-ht2416_integrin,_betasubunit
m24351_cds2_at_m24351_m24351,not_in_gb_record,_pthlh_gene_(parathyroid_hormone-
like_protein_a)_extra
m73489_3312-3660,heat-stable_enterotoxin_receptor_mrna,_complete_cds_
u73330exon_13-77,pac_85d2,_complete_sequence/gb=u73330/_ntype=dna/_annot=exon
- 20 x95425cds_2672-3061:in_reversesequence,_3810-3857,mrna_for_ehk-1_receptor_tyrosine_kinase_

Metagene 53
- k01160mrna_1077-1232,ii_histocompatibility_antigen_dc-alpha_chain_mrna_
25 m26041_1273-1405,mhc_ii_dq_alpha_mrna,_complete_cds
m63379mrna_1190-1646,trpm-2_protein_gene_
u38810_2191-2659,mab-21_cell_fate-determining_protein_homolog_(cagr1)_mrna,_complete_cds_

Metagene 33
- 30 hg1728-ht1734_at_hg1728-ht1734_non-specific_cross_reacting_antigen,_altsplice_form_2_
j04046mrna_1559-2089,calmodulin_mrna,_complete_cds_
s77835_88-380,_il-2=interleukin-2_[human,_brain,_mrna,_418_nt]/gb=s77835/_ntype=rna_
s83362mrna_10-109,_differentiation-
- 35 stimulating_factor/leukemia_inhibitory_factor_receptor_{5'_region
u65581_958-1420,ribosomal_protein_l3-like_mrna,_complete_cds.
x58234mrna_31-253,mrna_for_anti-lectin_antibody_epitope_(clone_p36/8-5)
- Metagene 184

- d13720_3754-4319,mrna_for_lyk_complete_cds
d30715mrna#3_3-198,_alternative_splicing;_type-2_mrna_frompap_(pancreatitis-associated_protein)_gene
- 5 139061mrna_1198-1654,transcription_factor_sl1_mrna_partial_cds_
m34276cds_2066-2228:in_reversesequence,_213-354,plasminogen_gene
u09178_3355-3898,dihydropyrimidine_dehydrogenase_mrna_complete_cds
u37707_2429-2969,dlg3_mrna_complete_cds_
u38291mrna_9685-10027,microtubule-associated_protein_1a_(map1a)_genomic_sequence
- 10 u66578cds_598-1036:in_reversesequence,_1277,putative_g_protein-coupled_receptor_(gpr23)_gene,_comple
u69263_474-1002,matrilin-2_precursor_mrna_partial_cds_
u79667_3199-3522,alpha1a-voltage-dependent_calcium_channel_mrna_splice_form_bi-1-v2-ggcag,_partial_
- 15 u87223_4830-5196,contactin_associated_protein_(caspr)_mrna_complete_cds_
x01388cds_14-272:in_reversesequence,_349-529,mrna_for_pre-apolipoprotein_ciii_
x66358cds#1_633-1041,mrna_kkialre_for_serine/threonine_protein_kinase
x75346cds_788-1157:in_reversesequence,_1205-
1305,mrna_for_map_kinase_activated_protein_kinase_
- 20 Metagene 419
- d13264_1681-2167,mrna_for_macrophage_scavenger_receptor_type_i,_3'_untranslated_region_
d38122_1307-1829,mrna_for_fas_ligand_complete_cds_
- 25 hg1686-ht4572_s_at_hg1686-
ht4572_transcription_factor_e4tfl_respiratory_gamma_subunit_altsplice_4_
u25029_1010-1556,glucocorticoid_receptor_alpha_mrna_variant_3'_utr
u34844exon_40-259,mercurial-insensitive_water-channel_gene,_5'_region_and_partial_exon/gb=u34844_/nt
- 30 u52191_4854-5396,smcy_(h-y)_mrna_complete_cds_
Metagene 331
- ac002045mrna#2_625-908,_a-589h1.1_fromchromosomebac_clone_cit987-ska-
589h1_~complete_genomic_sequenc
- 35 d10523_3533-4079,mrna_for_2-oxoglutarate_dehydrogenase_complete_cds_
d31840_3679-4148,drpla_mrna_for_orf_complete_cds
d50912_2685-3183,mrna_for_kiaa0122_gene_partial_cds_
d80008_2695-3205,mrna_for_kiaa0186_gene_complete_cds

- d86963_4563-5097,mrna_for_kiaa0208_gene_complete_cds_
d87078_4798-5296,mrna_for_kiaa0235_gene_partial_cds_
hg1612-ht1612_at_hg1612-ht1612_macmarcks_
hg2525-ht2621_at_hg2525-ht2621_helix-loop-helix_protein_delta_max_altsplice_1_
5 hg3635-ht3845_f_at_hg3635-ht3845_zinc_finger_protein_kruppel-like_
107648_1955-2321,mx11_mrna_complete_cds_
176702mrna_2447-3005,b56-delta_mrna_complete_cds_
m13452_1927-2435,lamin_a_mrna_3'_end
m91670_301-787,ubiquitin_carrier_protein_(e2-epf)_mrna_complete_cds_
10 s49592_1868-2425_transcription_factor_e2f_like_protein_[human,mrna_2492_nt]
u09820_5579-6058,helicase_ii_(rad54l)_mrna_complete_cds.
u22963_752-1238,i_histocompatibility_antigen-like_protein_mrna_complete_cds.
u34044_1143-1647,selenium_donor_protein_(seld)_mrna_complete_cds
u37012_3868-4372,cleavage_and_polyadenylation_specificity_factor_mrna_complete_cds
15 u52426_3469-3997,gok_(gok)_mrna_complete_cds
u54778_1131-1671,14-3-3_epsilon_mrna_complete_cds_
u57342_967-1459,myelodysplasia/myeloid_leukemia_factor(mlf2)_mrna_complete_cds_
u72761_2753-3233,karyopherin_betamrna_complete_cds/gb=u72761/_ntype=rna
u81984_2277-2739,endothelial_pas_domain_protein(epas1)_mrna_complete_cds_
20 all_x06323_1105-
1520,mrl3_mrna_for_ribosomal_protein_l3_homologue_(mrl3=_mammalian_ribosome_l3_)_
x71428mma_1284-1788,fus_mrna
x75755mma#1_1337-1471,pr264_gene_
all_x76717_3-268,mt-11_mrna
25 all_x83928_456-919,mrna_for_transcription_factor_ttfid_subunit_tafii28_
all_x90824_828-1337,mrna_for_usf2a_&_usf2b_clone_p9dh_
x97160mma_2016-
2532_tfe3_transcription_factor_gene_extracted_fromtfe3_gene_exons_1,2,3_(and_joine
y07595cds_948-
30 1344:in_reversesequence_1501,mrna_for_52_kd_subunit_of_transcription_factor_ttfih
y13247_3077-3581,fb19_mrna
y13620_5732-6182,mrna_for_bcl9_gene/gb=y13620/_ntype=rna
z37166cds_1006-1252:in_reversesequence_1432-
1570,bat1_mrna_for_nuclear_rna_helicase_(dead_family)
35
Metagene 295
u78551_838-1396,gallbladder_mucin_muc5b_mrna_partial_cds_

Metagene 183

105628_4400-4969,multidrug_resistance-associated_protein_(mrp)_mrna,_complete_cds

107541_950-1436,replication_factor_38-kda_subunit_mrna,_complete_cds

5 u28413_1440-

1926,cockayne_syndrome_complementation_group_a_csa_protein_(csa)_mrna,_complete_cds

Metagene 20

10 af008937_508-916,syntaxin-16c_mrna,_complete_cds/gb=af008937/_ntype=rna_

d90282_4830-5136,carbamyl_phosphate_synthetase_i_(ec_6.3.4.16)_mrna

hg2846-ht2983_at_hg2846-ht2983_dihydrofolate_reductase,_altsplice_6

l19161_1001-1385,translation_initiation_factor_eif-2_gamma_subunit_mrna,_complete_cds

l24804_223-721,(p23)_mrna,_complete_cds

15 l36463_2081-2627,ras_inhibitor_(rin1)_mrna,_complete_cds

l77701mrna_43-337,cox17_mrna,_complete_cds

m90356cds_222-618:in_reversesequence,_1194-

l281,btf3_protein_homologue_gene,_complete_cds_

u34301mrna_2-

20 35,nonmuscle_myosin_heavy_chain_iib_gene,_promoter_region_and_exon/gb=u34301/_ntype=dna

u47025_3462-3994,fetal_brain_glycogen_phosphorylase_b_mrna,_complete_cds_

u55936_367-757,snap-23_mrna,_complete_cds

u70322_2456-3014,transportin_(tm)_mrna,_complete_cds

x68836cds_653-1139,mrna_for_s-adenosylmethionine_synthetase

25 z18859mrna_933-

1461,cone_transducin_alpha_subunit_gene_extracted_fromgene_for_cone_transducin_alpha_

Metagene 383

30 l11005_4386-4878,aldehyde_oxidase_(haox)_mrna,_complete_cds

u81262_2433-2877,lerk-5_(lerk-5)_mrna,_complete_cds

all_x89426_1465-1958,mrna_for_esm-1_protein

Metagene 339

35

d42045_3927-4419,mrna_for_kiaa0086_gene,_complete_cds

all_m86933_669-

706,amelogenin_(amely)_mrna,_complete_cds,amelogenin_(amely)_mrna,_complete_cds

m96980_2034-2598,myelin_transcription_factor(mtf1)_mrna,_3'_end

all_x16282_710-1185,mrna_for_zinc_finger_protein_(clone_647)_
x89960cds_21-327:in_reversesequence,_458-698,mrna_for_mitochondrial_capsule_selenoprotein

Metagene 300

5

d15050_4757-5231,mrna_for_transcription_factor_areb6,_complete_cds_
hg3748-ht4018_at_hg3748-ht4018_basic_transcription_factor,_44_kda_subunit
s82472cds_3-
73,_beta_#name?_polymerase_beta_{exon_alpha_to_exon_vii_region}_[human,_genomic,_124_nt,

10

Metagene 291

af006609_5-189,rgs3_mrna,_5'_utr/gb=af006609_/ntype=rna_
d38491_298-808,mrna_for_kiaa0117_gene,_partial_cds_
15 d50924_3807-4083,mrna_for_kiaa0134_gene,_complete_cds
m86826_1501-2023,igf_binding_protein_complex_acid-labile_subunit_a_mrna,_complete_cds
m97252_5809-6271,kallmann_syndrome_(kal)_mrna,_complete_cds_
u27768_235-709,rgp4_mrna,_complete_cds_
u51127_1706-2084,interferon_regulatory_factor(humirf5)_mrna,_complete_cds_
20 u62961_2749-3241,succinyl_coa:3-oxoacid_coa_transferase_precursor_(oxct)_mrna,_complete_cds

Metagene 215

d67029_4839-5355,sec14l_mrna,_complete_cds_
25 m61916_5027-5582,laminin_b1_chain_mrna,_complete_cds_
m69225mrna_8371-8845,bullous_pemphigoid_antigen_(bpag1)_mrna,_complete_cds_
u10550_1591-2107,gem_gtpase_(gem)_mrna,_complete_cds_
u50928_4486-
4858,autosomal_dominant_polycystic_kidney_disease_type_ii_(pkd2)_mrna,_complete_cds
30 u73936_5049-5523,jagged(hj1)_mrna,_complete_cds_
u97105_4818-5364,n2a3_mrna,_complete_cds
x05908cds_814-1012:in_reversesequence,_1110-1338,mrna_for_lipocortin
all_x81895_791-1350,genx-5624_mrna,_3'_utr/gb=x81895_/ntype=rna

35 Metagene 109

hg1327-ht1327_s_at_hg1327-ht1327_statherin_
hg2723-ht2819_at_hg2723-ht2819_proto-oncogene_n-cym
hg3971-ht4241_at_hg3971-ht4241_transcription_factor

- hg4332-ht4602_at hg4332-ht4602_zinc_finger_protein_znfpt1
 107949_1619-2075,gnrh_receptor_mrna_complete_cds_
 m11722_1473-2037,terminal_transferase_mrna_complete_cds_
 m13143_1762-
- 5 2224_nucleotide_sequence_of_the_cdna_insert_of_lambda_pk129_coding_forplasma_prekallikr
 m83363_4104-4614,plasma_membrane_calcium-pumping_atpase_(pmca4)_mrna_complete_cds_
 s69369_779-1115_pax3a=transcription_factor_[human_adult_cerebellum_mrna_1248_nt]
 s69965_171-597_beta-synuclein_[human_brain_mrna_730_nt]
 u83117_1201-1477,sentrin_mrna_complete_cds
- 10 all_x64594_1290-1855,mrna_for_50_kda_erythrocyte_plasma_membrane_glycoprotein

Metagene 36

- hg2538-ht2634_at hg2538-ht2634_heterogeneous_nuclear_ribonucleoprotein_c_
 15 u43653_2816-3155,obese_protein_(ob)_mrna_complete_cds_
 v00532mrna_387-911_ifna_gene_(interferon_alpha-
 i)_extracted_fromgene_for_leukocyte_(alpha)_interfer
 all_z46632_2953-3206,hspde4c1_gene_for_3'_5'_-
 cyclic_amp_phosphodiesterase,hspde4c1_gene_for_3'_5'

20

Metagene 290

- d13540_1948-2500,mrna_for_protein-tyrosine_phosphatase_
 s83325_1796-2275_aspartyl(asparaginy)l)beta-
 25 hydroxylase_[human_hepatoblastoma_cell_line_hepg2_mrna
 all_x53296_1099-1657,mrna_for_irap_
 all_x95237_1357-1868,mrna_for_cysteine-rich_secretory_protein-1

Metagene 487

- 30 s76067cds_405-759_cng2=cyclic_nucleotide-
 gated_cation_channel_[human_peripheral_leucocytes_genomi
 u13021_844-1392,positive_regulator_of_programmed_cell_death_ich-11_(ich-
 1)_mrna_complete_cds
- 35 u72508_757-1105,b7_mrna_complete_cds
 x83490exon_3-34:in_reversesequence_389,mrna_for_fas/apo-1_(clone_pctrlm11-
 fasdelta(3,4))/gb=x83490_
 z31690cds_838-1129:in_reversesequence_1226-
 1445,(hepg2)_lal_mrna_for_lysosomal_acid_lipase_

Metagene 481

- 175847_1808-2330,zinc_finger_protein_45_(znf45)_mrna,_complete_cds_
5 176465_1929-2493,nad+-
 dependentlyhydroxyprostaglandin_dehydrogenase_(pgdh)_mrna,_complete_cds_
 m28585_329-839,leukocyte_interferon-alpha_mrna,_complete_cds,_clone_pifn105
 u50196_1238-1760,adenosine_kinase_mrna,_complete_cds_
 u92458_3747-4269,metabotropic_glutamate_receptormrna,_complete_cds

10

Metagene 355

- all_x85750_1935-
 2500,mrna_for_transcript_associated_with_monocyte_to_macrophage_differentiation
15 y09306cds_308-812,mrna_for_protein_kinase,_dyrk6,_partial/gb=y09306_/ntype=rna_

Metagene 289

- all_d29992_987-1132,mrna_for_placental_protein(pp5),_complete_cds_
20 m86849_1747-2179,connexin_26_(gjb2)_mrna_
 all_m96132_32-66,mhc_ii_hla-dr-beta-1*09012_(hla-dr1*09012)_gene,_3'_end_cds

Metagene 236

- 25** m11321mrna_1193-1703,group-specific_component_vitamin_d-
 binding_protein_mrna,_complete_cds_
 m58509cds#1_1114-1441:in_reversesequence,_4757-
 4867,_fdxr_gene_(adrenodoxin_reductase)_extracted_fro
 s57153_2388-
30 2878,_rbp1=retinoblastoma_binding_proteinisoform_i_{alternatively_spliced}_[human,_mrna_
 s79854_1585-
 1963,_typeiodothyronine_deiodinase=selenoenzyme_[human,_placenta,_mrna,_2066_nt]_
 u34360_3316-3832,lymphoid_nuclear_protein_(laf-4)_mrna,_complete_cds_
 all_v01515_5300-5550,gene_encoding_preproglucagonglucagon_is_a_29-
35 amino_acid_pancreatic_hormone_whic

Metagene 139

hg4518-ht4921_r_at_hg4518-ht4921_transcription_factor_btf3_homolog_

s81083mrna_3078-3438,<beta>-

add_gene_extracted_from_beta_#name?_beta_subunit_63_kda_isoform/membran

all_x86019_2045-2574,mrna_for_prpl-2_protein_

5 Metagene 72

j02986exon#3_1617-

1983_fgfr4_gene(transforming_protein)_extracted_fromtransforming_protein_(hst)_ge

m22489_1036-1504,bone_morphogenetic_protein_2a(bmp-2a)_mrna_

10 u63289_1548-2010,rna-binding_protein_cug-bp/hnab50_(nab50)_mrna,_complete_cds

Metagene 396

d14043_1834-2362,mrna_for_mgc-24,_complete_cds_

15 d26067_2680-3166,mrna_for_kiaa0033_gene,_partial_cds_

d29805_3485-3995,mrna_for_beta-1,4-galactosyltransferase,_complete_cds_

d29963mrna_885-1443,sfa-1(a_member_of_transmembranesuperfamily)_mrna,_complete_cds_

d30655_1263-1809,mrna_for_eukaryotic_initiation_factor_4aai

d43636_3576-4080,mrna_for_kiaa0096_gene,_partial_cds_

20 d50919_3864-4404,mrna_for_kiaa0129_gene,_complete_cds

d50926_3626-4124,mrna_for_kiaa0136_gene,_partial_cds_

d87446_5583-6135,mrna_for_kiaa0257_gene,_partial_cds_

d87685_5584-5920,mrna_for_kiaa0244_gene,_partial_cds_

j04058_767-1217,electron_transfer_flavoprotein_alpha-subunit_mrna,_complete_cds

25 l14837_7335-7839,tight_junction_(zonula_occludens)_protein_zo-1_mrna,_complete_cds_

l19872_4756-5059,ah-receptor_mrna,_complete_cds

l40027mrna_1586-2132,glycogen_synthase_kinase_mrna,_complete_cds

l40392mrna_1818-2280,(clone_sl64)_mrna,_3'_end_of_cds_

l48513mrna_941-1445,paraaxonase(pon2)_mrna,_complete_cds_

30 m20867_2463-2986,glutamate_dehydrogenase_(gdh)_mrna,_complete_cds

m29204mrna#1_2236-2782,dna-binding_factor_mrna,_complete_cds_

m31013mrna_4587-5091,nonmuscle_myosin_heavy_chain_(nmhc)_mrna,_3'_end

m62831mrna_1210-1750,transcription_factor_etr101_mrna,_complete_cds

m65217_1840-2278,heat_shock_factor(hsf2)_mrna,_complete_cds_

35 m77142_1629-2193,polyadenylate_binding_protein_(tia-1)_mrna,_complete_cds

m96954_806-1313,nucleolysin_tiar_mrna,_complete_cds_

s72008_1731-2229,hcdc10=cdc10_homolog_[human,_fetal_lung,_mrna,_2314_nt]_

s80562_1042-1582,acidic_calponin_[human,_kidney,_mrna,_1607_nt]

- u11313mrna_2104-2587,sterol_carrier_protein-x/sterol_carrier_protein-2_(scp-x/scp-2)_gene,_promoter_
u14588_3012-3570,paxillin_mrna,_complete_cds_
u23942_2811-3129,lanosterol_14-demethylase_cytochrome_p450_(cyp51)_mrna,_complete_cds
- 5 u31383_755-1151,g_protein_gamma-10_subunit_mrna,_complete_cds
u35113_2039-2555,metastasis-associated_mta1_mrna,_complete_cds_
u43077_964-1510,cdc37_homolog_mrna,_complete_cds_
u53209_968-1436,transformer-2_alpha_(htra-2_alpha)_mrna,_complete_cds
u61167_3488-4028,sh3_domain-containing_protein_sh3p18_mrna,_complete_cds_
- 10 u79267_987-1437,clone_23840_mrna,_partial_cds
u90909_944-1412,clone_23722_mrna_sequence
x04654cds_1467-1819:in_reversesequence,_2524-2634,mrna_for_u1_rna-associated_70k_protein_
all_x72727_2460-2794,tunp_mrna_for_transformation_upregulated_nuclear_protein
all_x76061_4282-4793,p130_mrna_for_130k_protein
- 15 x80230mrna_1187-1697,mrna_(clone_c-2k)_mrna_for_serine/threonine_protein_kinase
all_x87838_2803-3320,mrna_for_beta-catenin_
all_x98172_2240-2754,mrna_for_mach-alpha-1_protein_
all_z15115_2781-3346,top2_mrna_for_dna_topoisomerase_ii_(partial)
all_z24725_2759-3210,mitogen_inducible_gene_mig-2,_complete_cds
- 20 Metagene 351
- d38503_915-1455,pms8_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-terminal_regio
- 25 hg3313-ht3490_at_hg3313-ht3490_thyroid_hormone_receptor,_beta-2
hg3996-ht4266_at_hg3996-ht4266_cpg-enriched_dna,_clone_s21_
- Metagene 152
- 30 hg3115-ht3291_at_hg3115-ht3291_golli-mbp_
102950_673-1177,mu-crystallin_mrna,_complete_cds_
all_m10950_57-304,alpha-fetoprotein_(afp)_gene
m64572_3431-3923,protein_tyrosine_phosphatase_mrna,_complete_cds_
s68134_500-665,_crem=cyclic_amp-
- 35 responsive_element_modulator_beta_isoform_[human,_mrna,_1030_nt]
u41898_73-505,sodium_cotransporter_rkst1_mrna,_partial_cds/gb=u41898/_ntype=rna
u50708_946-1384,branched_chain_alpha-ketoacid_dehydrogenase_e1_beta_subunit_mrna,_complete_cds_

Metagene 420

- d14838_915-1317,mrna_for_fgf-9,_complete_cds_
 - d38548_4682-5210,mrna_for_kiaa0076_gene,_complete_cds
5 d63851_3157-3643,mrna_for_unc-18_homologue,_complete_cds_
 d87073_5307-5847,mrna_for_kiaa0236_gene,_complete_cds
 hg1728-ht1734_s_at_hg1728-ht1734_non-specific_cross_reacting_antigen,_altsplice_form_2_
 m28827_620-1112,thymocyte_antigen_cd1c_mrna,_complete_cds
 m92449_668-1190,ltr_mrna,_3'_end_of_coding_region_and_3'_flank_
10 u02388_2097-2337,cytochrome_p450_4f2_(cyp4f2)_mrna,_complete_cds_
 u59632_2578-
 3138,h5_mrna,_partial_cds,_and_platelet_glycoprotein_ib_beta_chain_mrna,_complete_cds
 u72517_413-
 953,alternatively_spliced_variant_c7f_(c3f)_mrna,_partial_3'_utr/gb=u72517_/ntype=rna_
15

Metagene 219

- d38462exon_57-
 549,gene_for_a1_chain_of_type_xix_collagen,_exon_+3'/gb=d38462_/ntype=dna_/annot=exon
20 120433_3738-3780,octamer_binding_transcription_factor(otf1)_mrna,_complete_cds
 z68204cds_43-373,mrna_for_succinyl_coa_synthetase/gb=z68204_/ntype=rna_
 Metagene 15

- 25** 129306_723-1116,tryptophan_hydroxylase_(tph)_mrna,_complete_cds/gb=129306_/ntype=rna
 all_m14159_1264-1482,_t-cell_receptor_beta-chain_j2.1_gene_extracted_fromt-
 cell_receptor_germline_be
 m20566mrna_2745-3180,interleukinreceptor_mrna,_complete_cds_
 s69232_1584-1992,_electron_transfer_flavoprotein-
30 ubiquinone_oxidoreductase_[human,_fetal_liver,_mrna
 u09851_44-254,zinc_finger_protein_(znf148)_mrna,_partial_cds_
 y07512_3211-3715,mrna_for_type_i_beta_cgmp-dependent_protein_kinase_(ec_2.7.1.37)
 all_z80779_563-822,h2b/g_gene

35 Metagene 11

hg2662-ht2758_at_hg2662-ht2758_homeotic_protein_emx1_
 109753_1377-1827,cd30_ligand_mrna,_complete_cds_
 s71018_282-798,_cyclophilin_c_[human,_kidney,_mrna,_883_nt]_

s76473_2563-3079, trkb [human, brain, mrna, 3194 nt]

Metagene 133

- 5 all_d00726_1842-2413, mrna_for_ferrochelatase (ec_4.99.1.1)_
d16217_1904-2414, mrna_for_calpastatin, complete_cds
d63390_600-1164, mrna_for_acetylhydrolase_ib_beta-subunit, complete_cds_
d87464_2481-2961, mrna_for_kiaa0274_gene, complete_cds
hg2850-ht4814_s_at_hg2850-ht4814_biliary_glycoprotein, altsplice_5, a
- 10 hg3578-ht3781_at_hg3578-ht3781_autoimmune_antigen, thyroid_disease-related_antigen_
hg417-ht417_s_at_hg417-ht417_cathepsin_b_
hg4234-ht4504_at_hg4234-ht4504_methylenetetrahydrofolate_reductase_
hg4660-ht5073_at_hg4660-ht5073_microtubule-associated_protein_1b_
hg945-ht945_s_at_hg945-ht945_nucleic_acid-binding_protein
- 15 j05213_430-958, sialoprotein_mrna, complete_cds_
l07033_967-1507, hydroxymethylglutaryl-coa_lyase_mrna, complete_cds_
l38486mrna_1162-1720, microfibril-associated_glycoprotein(mfap4)_mrna, 3'_end_of_cds_
m71243mrna_25-
38: not_in_gb_record, glycophorin_sta (type_a)_exonsand_4, partial/gb=m71243/_ntype=dna_
20 m76424gene_6565-7070, carbonic_anhydrase_vii_(ca_vii)_gene
u01824_1402-1912, glutamate/aspartate_transporter_ii_mrna, complete_cds_
u07000cds#4_558-810: in_reversesequence, 97660-
97876, bcr_gene_(unknown)_extracted_frombreakpoint_clu
u13044_1429-1945, nuclear_respiratory_factor-2_subunit_alpha_mrna, complete_cds_
25 u19948_1058-1616, protein_disulfide_isomerase_(pdip)_mrna, complete_cds_
u27831cds_1110-1578: in_reversesequence, 1602-1680, striatum-
enriched_phosphatase_(step)_mrna, partial
u44059_429-909, thyrotroph_embryonic_factor_(tef)_mrna, complete_cds
u49441_258-
30 648, mitochondrial_trifunctional_protein_beta_subunit_mrna, partial_cds/gb=u49441/_ntype=r
u51205_333-873, cop9_homolog_(hcop9)_mrna, complete_cds_
u59057_226-754, beta-a4_crystallin_(cryba4)_mrna, complete_cds
u59736_2496-2772, transcription_factor_(nfatc.b)_mrna, complete_cds_
u63455mrna_4412-4868, sulfonyleurea_receptor_(sur1)_gene_
35 u67988_1623-2163, guanylate_kinase_associated_protein_(gkap)_mrna, complete_cds_
u86358_296-818, chemokine_(teck)_mrna, complete_cds/gb=u86358/_ntype=rna
u90918_1794-2094, clone_23654_mrna_sequence_
u96769mrna_1266-1746, chondroadherin_gene, 5'_flanking_region_and_

- u96781mrna#1_2433-2961,atp2a1_gene_(ca2+_atpase_of_fast-twitch_skeletal_muscle_sacroplasmic_reticul
x65633cds_585-870:in_reversesequence,_1568-1766,acth-
r_gene_for_adrenocorticotrophic_hormone_receptor
- 5** x66114mrna_564-1074,gene_for_2-oxoglutarate_carrier_protein_
all_x77197_2631-3166,mrna_for_chloride_channel_
x83973cds_2262-2538:in_reversesequence,_2738-2822,mrna_for_ttf-i
x91117mrna_1655-2033,hg_net_gene_exon_1_
x92521cds_1127-1484:in_reversesequence,_1618-1768,mrna_for_mmp-19_protein_
- 10** x93996mrna_2570-3113,mrna_for_afx_protein_
x95406exon#1-2_12-17:not_in_gb_record,cyclin_e_gene.
y07847exon#3_36-582,mrna_for_rrp22_protein_
z71389mrna_85-295,mrna_for_skin-antimicrobial-peptide(sap1).
- 15** Metagene 61
- m31166mrna_1286-1784,tumor_necrosis_factor-inducible_(tsg-14)_mrna,_complete_cds_
u60415_2126-2570,bhlh-pas_protein_jap3_mrna,_complete_cds
u70981_749-1283,interleukin-13_receptor_mrna,_complete_cds_
20 z83803_7-259,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc4)
- Metagene 463
- hg2709-ht2805_at_hg2709-ht2805_serine/threonine_kinase_
25 hg3137-ht3313_at_hg3137-ht3313_zinc_finger_protein_znf81_
hg4052-ht4322_at_hg4052-ht4322_glutamate_ionotropic_receptor
m13666_800-992,c-myb_mrna,_3'_end
m15656cds_712-1066:in_reversesequence,_3992-4082,aldolase_b_(aldob)_gene
m54995_108-603,connective_tissue_activation_peptide_iii_mrna,_complete_cds_
30 s69790_962-1412,_brush-
l=tumor_suppressor_{3'_region}_[human,_breast_epithelium,_mrna_partial,_1485_
all_x53065_85-462,spr2-1_gene_for_small_proline_rich_protein_(exon_2)
y10571cds_696-978:in_reversesequence,_1002-1194,mrna_for_ding_gene
all_y11897_19-320,brx_gene_3'_utr/gb=y11897_/ntype=rna_
35 z75330cds_3384-3714:in_reversesequence,_4156-4312,mrna_for_nuclear_protein_sa-1.
- Metagene 414
- d86640_2374-2902,mrna_for_stac,_complete_cds_

- hg2157-ht2227_at_hg2157-ht2227_mucin_4,_tracheobronchial_
j03507_3421-3865,complement_protein_component_c7_mrna,_complete_cds
all_115296_3031-3082,clone_hrcnc2b_retinal_rod_cyclic_nucleotide-
gated_cation_channel_gene,_complete
- 5 141390exon#1_244-395,corebeta-1,6-n-
acetylglucosaminyltransferase_(coregnt)_gene,_exon/gb=141390_/nt
m59820mrna_2435-2975,granulocyte_colony-
stimulating_factor_receptor_(csf3r)_mrna,_complete_cds_
m77481mrna_1021-1566,antigen_(mage-1)_gene,_complete_cds
- 10 m82962mrna_2313-2835,n-benzoyl-l-tyrosyl-p-amino-
benzoic_acid_hydrolase_alpha_subunit_(pph_alpha)_mr
m87284_2479-2923,69_kda_2'_5'_oligoadenylate_synthetase_(p69_2-
5a_synthetase)_mrna,_complete_cds_
u05291_1363-1849,fibromodulin_mrna,_partial_cds
- 15 u29589exon_2948-3488,m3_muscarinic_acetylcholine_receptor_(chrm3)_gene,_complete_cds_
u43672_2939-3443,putative_transmembrane_receptor_il-1rrp_mrna,_complete_cds
u71601_960-1422,zinc_finger_protein_zfp47_(zf47)_mrna,_partial_cds_
x06482cds_60-405:in_reversesequence,_884-887,theta_1-globin_gene
all_x14975_7566-8337,cd1_r2_gene_for_mhc-related_antigen_
20 x55989mrna_169-354,ecrp_gene_for_eosinophil_cationic_related_protein
y10512mrna_14-452,mrna_for_cd282_protein/gb=y10512_/ntype=rna
- Metagene 113
- 25 110102mrna#1_392-794,sex-determining_region_y_(sry)_gene,_complete_cds_
l34081mrna_1055-1601,bile_acid_coa:_amino_acid_n-acyltransferase_mrna,_complete_cds
m34353_6763-7342,transmembrane_tyrosine-specific_protein_kinase_(ros1)_mrna,_complete_cds
m61156_1122-1308,activator_protein_2b_(ap-2b)_mrna,_complete_cds_
m95767_1065-1563,di-n-acetylchitobiase_mrna,_complete_cds_
30 all_x02956_1039-1253,interferon_alpha_gene_ifn-alpha_5_
all_x07994_5703-6244,mrna_for_lactase-phlorizin_hydrolase_lph_(ec_3.2.1.23-62)_
x68994exon_4-55,creb_gene,_exon_y
all_x78686_706-1121,ena-78_mrna
all_x95239_863-1362,mrna_for_cysteine-rich_secretory_protein-2/type_i
35 y10508mrna_370-660,mrna_for_cd190_protein/gb=y10508_/ntype=rna_
y10508mrna_370-660,mrna_for_cd190_protein/gb=y10508_/ntype=rna_
- Metagene 106
- hg2007-ht2056_s_at_hg2007-ht2056_proto-oncogene_sno,_altsplice_n_

Metagene 319

- d42072_2020-2542,mrna_for_nfl_n-isoform-exon11,_complete_cds_
- 5 hg3998-ht4268_at_hg3998-ht4268_l-glycerol-3-phosphate:nad+_oxidoreductase
m28170_1894-1987,cell_surface_protein_cd19_(cd19)_gene,_complete_cds_
m62843_906-
1404,brain_protein_recognized_by_the_sera_of_patients_with_paraneoplastic_sensory_neurono
s67247_365-
- 10 821,_smooth_muscle_myosin_heavy_chain_isoform_smemb_[human,_umbilical_cord,_fetal_aorta,_
u08006exon#1_78-567,complementalpha_subunit_(c8a)_gene
u09411_1794-2343,zinc_finger_protein_znf132_mrna,_complete_cds_
u40343_657-1119,cdk_inhibitor_p19ink4d_mrna,_complete_cds
u52827_1022-1508,cri-du-chat_region_mrna,_clone_nibb11_
- 15 u66052mrna_7-271,clone_w2-6_mrna_from_chromosome_x/gb=u66052_/ntype=rna
x07173cds_2503-2803:in_reversesequence,_2956-3028,mrna_for_second_protein_of_inter-alpha-
trypsin_inh
x16316cds_2109-2355:in_reversesequence,_2483-2693,mrna_for_vav_oncogene_
x63578mrna_31-535,gene_for_parvalbumin

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Metagene 170

- 109230_933-1460,c-c_chemokine_receptor_type(c-c_ckr-1)_mrna,_complete_cds_
147276_383-934,(cell_line_hl-60)_alpha_topoisomerase_truncated-
25 form_mrna,_3'_utr/gb=147276_/ntype=rn
m13150mrna_776-1337,mass_proto-oncogene_mrna,_complete_cds
m20137mrna_400-820,interleukin(il-3)_mrna,_complete_cds,_clone_pcd-sr-alpha_
u33202_104-354,mdm2-d_(mdm2)_mrna,_complete_cds/gb=u33202_/ntype=rna_
all_x66894_3881-4417,facc_mrna_from_complementation_group_c_(fa(c))
30 all_y08263_1373-1902,mrna_for_aad14_protein,_partial_
all_y09980_16580-17121,hoxd3_gene_

Metagene 75

- 35 hg1227-ht1227_s_at_hg1227-ht1227_collagen_type_ii_alpha_1
all_j00116_4597-4806,alpha-1(ii)_collagen_gene_col2a1,_partial_cds_
m60299exon_73-163,alpha-
1_collagen_type_ii_gene,_exons_1,and/gb=m60299_/ntype=dna_/annot=exon
u14550_1319-1877,sialyltransferase_sthm_(sthm)_mrna,_complete_cds

u22322_2205-2587,nuclear_tyrosine_protein_kinase_rak_mrna,_complete_cds_
all_x57830_2409-3016,serotonin_5-ht2_receptor_mrna_

Metagene 223

5

all_m60749_829-1061,histone_h4_(h4)_gene,_complete_cds_
u24577_1182-1512,ldl-phospholipase_a2_mrna,_complete_cds_

Metagene 116

10

d63412_1299-1713,mrna_for_aquaporin,_complete_cds
hg2981-ht3938_s_at_hg2981-ht3938_epican,_altsplice_12
u61849_4650-5040,neuronal_pentraxin(nptx1)_mrna,_complete_cds_

15 Metagene 332

l37362_1009-1579,(clone_d2-115)_kappa_opioid_receptor_(oprk1)_mrna,_complete_cds
all_m28879_3325-4444,granzyme_b(ctla-1)_gene,_complete_cds
u34070cds_744-1053:in_reversesequence,_1731-
20 1763,ccaat/enhancer_binding_protein_alpha_gene,_complete
u57592_3563-4043,jumonji_putative_protein_(jumonji)_mrna,_complete_cds_
u93867_1248-
1764,rna_polymerase_iii_subunit_(rpc62)_mrna,_complete_cds/gb=u93867/_ntype=rna
all_z28339_2084-2649,mrna_for_delta_4-3-oxosteroidbeta-reductase

25

Metagene 196

d37984_1856-2314,mrna_for_dna_helicase_q1,_partial_cds_
l22214_2335-2857,adenosine_a1_receptor_(adoral)_mrna_exons_1-6,_complete_cds_
30 u17743_699-1221,jnk_activating_kinase_(jnk1)_mrna,_complete_cds_
u21051mrna#1_2326-2647,g_protein-coupled_receptor_(gpr4)_gene,_complete_cds_
u45975_882-1434,phosphatidylinositol_(4,5)bisphosphate_5-
phosphatase_homolog_mrna,_partial_cds_
u50743_13-439,na,k-atpase_gamma_subunit_mrna,_complete_cds_

35

Metagene 150

d17390_2313-2829,mrna_for_mdc_protein
d49410exon_48-534,gene_for_interleukinreceptor_alpha_subunit

- hg3063-ht3224_at_hg3063-ht3224_major_histocompatibility_complex_i_
hg3355-ht3532_at_hg3355-ht3532_peroxisome_proliferator_activated_receptor
hg4417-ht4687_f_at_hg4417-ht4687_homeotic_protein_hpx-2
111931_1454-1644,cytosolic_serine_hydroxymethyltransferase_(shmt)_mrna,_complete_cds_
5 m21056cds_193-403:in_reversesequence,_165-345,pancreatic_phospholipase_a-2_(pla-2)_gene_
m76231_292-790,sepiapterin_reductase_mrna,_complete_cds
m81379_1126-1546,alpha-3_type_iv_collagen_(col4a3)_mrna,_3'_end
m86383_1007-1527,nicotinic_acetylcholine_receptor_alphasubunit_mrna,_complete_cds_
m86407_2299-2833,alpha_actinin(actn3)_mrna,_complete_cds_
10 m95678_3990-4494,phospholipase_c-beta-2_mrna,_complete_cds
u06643_71-463,keratinocyte_lectin(hkl-14)_mrna,_complete_cds.
u16127_3025-3589,glutamate/kainate_receptor_subunit_(eaa5)_mrna,_complete_cds
u43142_1456-1972,vascular_endothelial_growth_factor_related_protein_vrp_mrna,_complete_cds_
u59913_1640-2168,chromosomemad_homolog_smad5_mrna,_complete_cds_
15 u62437_1943-2393,nicotinic_acetylcholine_receptor_beta2_subunit_precursor,_mrna,_complete_cds
u71300_1307-
1703,snrna_activating_protein_complex_50kd_subunit_(snap50)_mrna,_complete_cds_
all_x15217_2292-2875,sno_oncogene_mrna_for_snoa_protein,_ski-related_
all_x54741_2389-2918,cypxib2_gene_for_aldosterone_synthase_
20 x60592mrna_415-973,cdw40_mrna_for_nerve_growth_factor_receptor-related_b-
lymphocyte_activation_molec
x60655mrna_990-1474,evx1_mrna
x62891mrna_57-390,mutant_coseg_gene_for_vasopressin-neurophysin_precursor
x91257_1281-1797,mrna_for_seryl-trna_synthetase
25 x92475_905-1295,mrna_for_itba1_protein_
x95191cds_707-848,mrna_for_delta-sarcoglycan/gb=x95191_/ntype=rna
all_y11215_971-1446,mrna_for_skap55_protein/gb=y11215_/ntype=rna
z22865cds_164-578:in_reversesequence,_620,dermatopontin_mrna,_complete_cds
reverse_z49155_27087-
30 27346,dna_from_cosmid_l83d3,_huntington's_disease_region,_chromosome_4p16.3_

Metagene 263

ab003698_2634-3138,mrna_for_cdc7-related_kinase,_complete_cds
35 m77140_91-409,pro-galanin_mrna,_3'_end_
m98447mrna_2256-2670,keratinocyte_transglutaminase_gene,_complete_cds_
u23752_1679-1919,sox-11_mrna,_complete_cds

Metagene 282

- aj001421cds_117-567:in_reversesequence,_585-
600,mrna_for_rer1_protein/gb=aj001421/_ntype=rna_
d86981_5936-6410,mrna_for_kiaa0228_gene,_partial_cds_
- 5** 142452mrna_1100-1520,pyruvate_dehydrogenase_kinase_isoenzyme(pdk3)_mrna,_complete_cds
m22632mrna_1744-2284,mitochondrial_aspartate_aminotransferase_mrna,_complete_cds_
m87503_1085-1535,ifn-responsive_transcription_factor_subunit_mrna,_complete_cds
u01923_1649-2090,btk_region_clone_ftp-3_mrna_
u02081_1642-2026,guanine_nucleotide_regulatory_protein_(net1)_mrna,_complete_cds_
10 u04285utr#1_689-1148,lysosomal_acid_lipase,_cholesteryl_ester_hydrolase_(lipa)_gene
u16799_865-1419,na,k-atpase_beta-1_subunit_mrna,_complete_cds
u40038_1236-1425,gtp-binding_protein_alpha_q_subunit_(gnaq)_mrna,_complete_cds_
u53445_2442-
2928,ovarian_cancer_downregulated_myosin_heavy_chain_homolog_(doc1)_mrna,_complete_cds_
15 u58046_4637-5176,p167_mrna,_complete_cds_
u76421_4572-4962,dsrna_adenosine_deaminase_drada2b_(drada2b)_mrna,_complete_cds
u77718_2100-2592,desmosome_associated_protein_pinin_mrna,_complete_cds_
u81006_1886-2348,p76_mrna,_complete_cds
u89505_1087-1537,hlark_mrna,_complete_cds
20 u94586_145-445,nadh:ubiquinone_oxidoreductase_mlrq_subunit_mrna,_complete_cds
all_x01060_4427-4986,mrna_for_transferrin_receptor_
all_x13916_14416-14876,mrna_for_ldl-receptor_related_protein_
x53586mrna_4766-
5306_integrin_alpha(or_alpha_e)_protein_gene_extracted_frommrna_for_integrin_alpha_
25 all_x68560_2909-3480,spr-2_mrna_for_gt_box_binding_protein_
x69978cds_3218-3494:in_reversesequence,_3769-3781,mrna_for_xp-g_factor
all_x71490_1059-1552,mrna_for_vacuolar_proton_atpase,_subunit_d
all_x72790_30-1461,endogenous_retrovirus_mrna_for_orf/gb=x72790/_ntype=rna_
x77909cds_888-1122:in_reversesequence,_1202-1406,ikbl_mrna
30 x82676_3333-3873,mrna_for_tyrosine_phosphatase_
all_y00757_629-1134,mrna_for_polypeptide_7b2_
all_z34975_2303-2862,ldlc_mrna_
z49989cds_779-1079:in_reversesequence,_1540,mrna_for_smoothelin_

35 Metagene 85

d38553_2125-2665,mrna_for_kiaa0074_gene,_partial_cds_
d78367_1372-1810,mrna_for_k12_keratin,_complete_cds
j03133_2096-2612,transcription_factor_sp1_mrna,_3'_end_

- 106895_503-977,antagonizer_of_myc_transcriptional_activity_(mad)_mrna,_complete_cds_
 141816mrna_891-1389,cam_kinase_i_mrna,_complete_cds_
 s78085_719-1187,_pdc2=programmed_cell_death-
 2/rp8_homolog_[human,_fetal_lung,_mrna,_1282_nt]_
- 5** all_u66083_2217-
 2758,contig_of_two_cosmids_from_llnl_x_chromosome_library_(u83f1,_u109h10),_includin
 u89916_375-879,putative_osp_like_protein_mrna,_partial_cds
 all_x62048_1820-2343,weel_hu_gene
- 10** Metagene 385
 m32402mrna_1851-2253,placental_protein_(pp11)_mrna,_complete_cds_
 m93107_978-1278,heart_(r)-3-hydroxybutyrate_dehydrogenase_mrna,_3'_end
- 15** Metagene 465
 af015913_1437-1947,skblhs_mrna,_complete_cds/gb=af015913/_ntype=rna_
 d11428_1253-1757,mrna_for_pmp-22(pas-ii/sr13/gas-3)_of_peripheral_myelin,_complete_cds_
 d16294_1019-1523,mrna_for_mitochondrial_3-oxoacyl-coa_thiolase,_complete_cds_
20 d21063_2853-3303,mrna_for_kiaa0030_gene,_partial_cds_
 d38524_2673-3213,mrna_for_5'-nucleotidase_
 d63476_4587-4953,mrna_for_kiaa0142_gene,_complete_cds
 hg1827-ht1856_s_at_hg1827-ht1856_cytochrome_p450,_subfamily_iic,_altsplice_form_2
 hg2981-ht3127_s_at_hg2981-ht3127_epican,_altsplice_11
25 hg3521-ht3715_at_hg3521-ht3715_ras-related_protein_rap1b_
 j05682_1023-1575,subunit_c_of_v-atpase_(vat_c)_mrna,_3'_end
 l28997_443-953,arl1_mrna,_complete_cds
 l31801_2229-2535,monocarboxylate_transporter(slc16a1)_mrna,_complete_cds_
 m25753mrna_1103-1427,cyclin_b_mrna,_3'_end_
30 all_m27161_6940-7265,mhc_i_cd8_alpha-chain_(leu-2/t8)_gene,_complete_cds_
 m67468_3244-3720,fragile_x_mental_retardationfmr-1_gene,_3'_end,_clones_bc72_and_bc22_
 m74524_1190-1658,hhr6a_(yeast_radhomologue)_mrna,_complete_cds
 m90656_2044-2590,gamma-glutamylcysteine_synthetase_(gcs)_mrna,_complete_cds
 u00001_2019-2547,homologue_of_spombe_nuc2+_and_anidulans_bima
35 u01833_690-1164,nucleotide-binding_protein_mrna,_complete_cds
 u09564_3725-4205,serine_kinase_mrna,_complete_cds
 u15128cds_1011-1299:in_reversesequence,_2065-2233,beta-1,2-n-
 acetylglucosaminyltransferase_ii_(mgat2
 u17714_2774-3068:not_in_gb_record,putative_tumor_suppressor_(snc6)_mrna,_complete_cds_

- u27460_1582-1798,uridine_diphosphoglucose_pyrophosphorylase_mrna_complete_cds_
u39318_159-675,e2_ubiquitin_conjugating_enzyme_ubch5c_(ubch5c)_mrna_complete_cds_
u61145_2035-2509,enhancer_of_zeste_homolog(ezh2)_mrna_complete_cds_
u61232_1407-1869,tubulin-folding_cofactor_e_mrna_complete_cds_
5 u69141_1311-1719,glutaryl-coa_dehydrogenase_mrna_complete_cds_
u72263_2410-
2931,multiple_exostoses_type_ii_protein_ext2.i_mrna_complete_cds/gb=u72263_/ntype=rna_
u88047_1567-1969,dna_binding_protein_homolog_(drx)_mrna_partial_cds_
all_x02160_4717-4976,mrna_for_insulin_receptor_precursor_
10 all_x54993_1096-1685,tfiid_mrna
all_x56807_2617-3194,dsc2_mrna_for_desmocollins_type_2a_and_2b_
x59244mrna_2391-2967,znf43_mrna
x61100mrna_1983-
2445,_75_kda_subunit_nadh_dehydrogenase_precursor_gene_extracted_frommrna_for_mitoch
15 all_x63468_2398-2915,mrna_for_transcription_factor_tfiie_alpha_
all_x64229_888-1393,dek_mrna_
x65867cds#1_1157-1409:in_reversesequence,_1447-1639,mrna_for_adenylosuccinate_lyase_
all_x79201_2342-2775,mrna_for_syt
x85753_1268-1646,mrna_for_cdk8_protein_kinase
20 y00971mrna_1891-
2419,mrna_for_phosphoribosyl_pyrophosphate_synthetase_subunit_ii_(ec_2.7.6.1)_
y09943cds_117-452:in_reversesequence,_561-602,mrna_for_ngf-inducible_pc3_anti-
proliferative_protein_
25 Metagene 411

d17570_565-1083,mrna_for_zona-pellucida-binding_protein_(sp38),_complete_cds.
d49394_1619-2123,mrna_for_serotonin_5-ht3_receptor,_complete_cds_
hg2358-ht4858_s_at_hg2358-ht4858_proto-oncogene_ets-1,_altsplice_2_
30 l39833_2587-3097,(clone_hkvbeta3)_k+_channel_beta_subunit_mrna_complete_cds_
m13577mrna_1550-2096,myelin_basic_protein_(mbp)_mrna_complete_cds_
m14113mrna_8440-8986,coagulation_factor_viii:c_mrna_complete_cds_
all_m33987_2226-2701,carbonic_anhydrase_i_(cai)_mrna_complete_cds_
m35296_3284-3758,tyrosine_kinase_arg_gene_mrna_
35 m64934_1917-2397,kell_blood_group_protein_mrna_
all_s71129_3-426,_acetylcholinesterase_{i4-
e5_doman}_[human,tumor_cell_lines,genomic,_847_nt]_
s78234_2755-3259,nuc2_homolog_[human,fibroblasts,mrna,_3320_nt]
u00238_3024-3552,glutamine_prpp_amidotransferase_(gpat)_mrna_complete_cds

- u00943_1017-1203,clone_a9a2brb2_(cac)n/(gtg)n_repeat-containing_mrna_
u03397_787-1358,receptor_protein_4-1bb_mrna_complete_cds
u15460_322-844,bzip_protein_b-atf_mrna_complete_cds_
u27326_1666-
- 5** 2123,alpha_(1,3/1,4)_fucosyltransferase_(fut3)_mrna_major_transcript_i_complete_cds
u31875_979-1399,hep27_protein_mrna_complete_cds.
u40846_1964-2399,alpha-n-acetylglucosaminidase_(nag)_mrna_complete_cds
u51477_2883-3444,diacylglycerol_kinase_zeta_mrna_complete_cds_
u62317mrna#6_1634-
- 10** 2156,hypothetical_protein_384d8gene_extracted_from_chromosome_22q13_bac_clone_cit
u71364_1097-1553,serine_proteinase_inhibitor_(p19)_mrna_complete_cds
all_u73167_4971-
35099_h_luca14.2a_gene_extracted_fromcosmid_luca14_h_luca14.2a_gene_extracted_from
u79274_883-1381,clone_23733_mrna_complete_cds.
- 15** v00574cds_225-538:in_reversesequence,_3330-
3468,germ_line_gene_homologous_to_bladder_carcinoma_oncog
all_x17622_3693-4210,hbk2_mrna_for_potassium_channel_protein_
x51688mrna_1054-1438,mrna_for_cyclin_a_
all_x62515_13260-13708,mrna_for_basement_membrane_heparan_sulfate_proteoglycan_
- 20** x70040cds_3944-4130:in_reversesequence,_4236-4470,ron_mrna_for_tyrosine_kinase_
x85781exon_2-551,nos2_gene_exon_27/_gb=x85781/_ntype=dna/_annot=exon
y10055cds_2802-3096:in_reversesequence,_3310-3532,mrna_for_phosphoinositide_3-kinase_
- Metagene 326
- 25** 110035_162-666:in_reversesequence,_684-690,crystallin_beta-b2_mrna_complete_cds
m16594_790-904,glutathione_s-transferase_ha_subunit(gst)_mrna_complete_cds_
u81523_1378-1870,endometrial_bleeding_associated_factor_mrna_complete_cds.
all_y10375_1179-1706,mrna_for_sirp-alpha1
- 30** Metagene 237
- d17427_3421-3506,mrna_for_desmocollin_type_4_
d25278_2024-2510,mrna_for_kiaa0036_gene_complete_cds
- 35** d26528_1017-1515,mrna_for_rna_helicase_complete_cds_
d32202_2017-2263,mrna_for_alpha_1c_adrenergic_receptor_isoform_2_complete_cds_
d43768_663-1197,_numan_mrna_for_scm-1_(single_cysteine_motif-1)_complete_cds_
all_d49742_2413-2984,mrna_for_hgf_activator_like_protein_complete_cds_

- d49817_1233-1725,mrna_for_fructose_6-phosphate,2-kinase/fructose_2,6-bisphosphatase,_complete_cds
d49950_495-918,liver_mrna_for_interferon-gamma_inducing_factor(igif),_complete_cds_
d64158_415-
- 5 668:not_in_gb_record,mrna_for_atp_binding_protein_associated_with_cell_differentiation,_p
d82061_357-876,b-cell_mrna_for_a_member_of_the_short-chain_alcohol_dehydrogenase_family,_partial_cds
d82343_474-960,mrna_for_amy,_complete_cds
d88270exon#2_89-293:in_reversesequence,_18899-
- 10 19103,(lambda)_dna_for_immunoglobulin_light_chain
hg1804-ht1829_at_hg1804-ht1829_ornithine_aminotransferase-like
hg2367-ht2463_s_at_hg2367-ht2463_trithorax_homolog_hrx_
hg2416-ht2512_at_hg2416-ht2512_gal_beta_1,3(4)glnac_alpha2,3-sialyltransferase
hg2562-ht2658_s_at_hg2562-ht2658_a-myb_
- 15 hg2689-ht2785_at_hg2689-ht2785_mucin_5b,_tracheobronchial
hg3364-ht3541_at_hg3364-ht3541_ribosomal_protein_l37_
hg4102-ht4372_at_hg4102-ht4372_n-ethylmaleimide-sensitive_factor_
hg4115-ht4385_at_hg4115-ht4385_olfactory_receptor_or17-210_
hg4333-ht4603_at_hg4333-ht4603_zinc_finger_protein_znfpt7
- 20 hg961-ht961_at_hg961-ht961_guanine_nucleotide_exchange_factor_
j00073exon#2_132-255:not_in_gb_record,alpha-cardiac_actin_gene,_5'_flank_and
j00306cds_40-304:in_reversesequence,_1168-2537,somatostatin_i_gene_and_flanks_
l40371mrna_661-1075,thyroid_receptor_interactor_(trip4)_mrna,_3'_end_of_cds_
l42354mrna_25-409,(clone_48es4)_mrna_fragment/gb=l42354_/ntype=rna
- 25 l42451mrna_947-1397,pyruvate_dehydrogenase_kinase_isoenzyme(pdk2)_mrna,_complete_cds_
l77559mrna_55-403,dgs-b_partial_mrna/gb=l77559_/ntype=rna_
m12963mrna_871-985,i_alcohol_dehydrogenase_(adh1)_alpha_subunit_mrna,_complete_cds_
m14091mrna_1209-1731,thyroxine-binding_globulin_mrna,_complete_cds_
m14123cds#2_830-1280,_pol_fromendogenous_retrovirus_herv-
- 30 k10/gb=m14123_/ntype=dna_/annot=cds,_pol_fr
m14123cds#3_13-175,_pol_fromendogenous_retrovirus_herv-
k10/gb=m14123_/ntype=dna_/annot=cds,_pol_from
m25629_270-846,kallikrein_mrna,_complete_cds,_clone_clone_phkk25_
m25809_1358-1817,endomembrane_proton_pump_subunit_mrna,_complete_cds_
m26958_46-235,parathyroid_hormone-related_protein_(pthrp)_mrna,_5'_flank,_clone_pbrf52/gb=m26958_/nt
- 35 m29194cds_1090-1408:in_reversesequence,_175-223,triglyceride_lipase_gene
m29994exon#1_2-80,alpha-i_spectrin_gene,_exon/gb=m29994_/ntype=dna_/annot=exon_
m31241_s_at_m31241_m31241,not_in_gb_record,complement_receptor(cr1)_gene_

- m60721mrna_1630-2182,homeobox_gene_complete_cds_
m62982_1795-2299,arachidonate_12-lipoxygenase_mrna_complete_cds_
m63603_1052-1574,phospholamban_mrna_complete_cds
m63928_645-1161,t_cell_activation_antigen_(cd27)_mrna_complete_cds_
5 m74093_1283-1685,cyclin_mrna_
m83664_1098-1416,mhc_ii_lymphocyte_antigen_(hla-dp)_beta_chain_mrna_complete_cds
m89914_8414-8952,neurofibromin_(nfl)_gene_complete_cds
m93283_898-1438,pancreatic_lipase_related_protein(plrp1)_mrna_complete_cds_
m99438_1768-2332,transducin-like_enhancer_protein_(tle3)_mrna_complete_cds
10 s69115_250-808,_granulocyte_colony-
stimulating_factor_induced_gene_[human_cml_patient_bone_marrow_
s76756_510-954,_4r-map2=microtubule-
associated_protein4r_isoform_[human_brain_mrna_partial_1012_n
u00944_1121-1619,clone_a9a2brb6_(cac)n/(gtg)n_repeat-containing_mrna_
15 u04806_247-787,flt3/flk2_ligand_mrna_complete_cds.
u09367_1942-2449,zinc_finger_protein_znf136
u20230exon_7-127,guanyl_cyclase_c_gene_partial_cds/gb=u20230_/ntype=dna_/annot=exon_
u23430exon_172-496:in_reversesequence,_793-994,cholecystokinin_type_a_receptor_(cck-a)_gene
u33052_2643-3212,lipid-activated,_protein_kinase_prk2_mrna_complete_cds_
20 u34038_880-1390,proteinase-activated_receptor-2_mrna_complete_cds_
u37143_1256-1832,cytochrome_p450_monooxygenase_cyp2j2_mrna_complete_cds_
all_u37219_2132-2583,cyclophilin-like_protein_cyp-60_mrna_complete_cds
u40223cds_660-
1068:in_reversesequence,_1548,uridine_nucleotide_receptor_(unr)_gene_complete_cds
25 u47011mrna#1_581-791:in_reversesequence,_751-
961,_fgf8_gene_(fibroblast_growth_factorprecursor)_extr
u48707_123-597,protein_phosphatase-1_inhibitor_mrna_complete_cds
u50527_1493-1891,brca2_region_mrna_sequence_cg018_
u59286_49-439,beta-r1_mrna_partial_cds/gb=u59286_/ntype=rna_
30 u59321_1625-1967,dead-box_protein_p72_(p72)_mrna_complete_cds_
u60519_2965-3499,apoptotic_cysteine_protease_mch4_(mch4)_mrna_complete_cds
u66048mrna_2400-2838,clone_161455-2-3_b_cell_expressed_mrna_from_chromosome_x
u66088_1895-2369,sodium_iodide_symporter_mrna_complete_cds
u71088_1325-1586,map_kinase_kinase_mek5c_mrna_complete_cds
35 u75272_743-1283,gastriecin_mrna_complete_cds
u75276_2760-3225,tifib_related_factor_hbrf_(hbrf)_mrna_complete_cds.
u79115_337-886,death_adaptor_molecule_raidd_(raidd)_mrna_complete_cds.
u79253_734-1100,clone_23893_mrna_complete_cds.

- u90306_13-175,iroquois-class_homeodomain_protein_irx-
4_mrna_partial_cds/gb=u90306_/ntype=rna
u96629mrna#1_1142-
1658_2a8.2_gene_(unknown_protein_cit987sk_2a8_1)_extracted_fromchromosomebac_clon
- 5** all_x00588_5021-5514,mrna_for_precursor_of_epidermal_growth_factor_receptor
x02612mrna#3_656-1184,gene_for_cytochrome_p(1)-450_
all_x03663_3391-3824,mrna_for_c-fms_proto-oncogene_
x17254cds_911-1211:in_reversesequence,_1335-1449,mrna_for_the_transcription_factor_eryfl
x54673cds_1493-1775:in_reversesequence,_2015-2135,gat1_mrna_for_gaba_transporter
- 10** all_x65873_3040-3551,mrna_for_kinesin_(heavy_chain)
x65977cds_118-268:in_reversesequence,_325-499,mrna_for_corticostatin_hp-4_precursor_
all_x74301_4170-4479,mrna_for_mhc_ii_transactivator
all_x78416_369-921,alpha-s1-casein_mrna
all_x80878_4120-4349,r_kappa_b_mrna
- 15** all_x82895_2890-3425,mrna_for_dlg2_
x95190cds_1574-1958:in_reversesequence,_2170,mrna_for_branched_chain_acyl-coa_oxidase_
x97302mrna_40-235,mrna_for_ptg-1_protein/gb=x97302_/ntype=rna
x99393cds_292-552:in_reversesequence,_655-787,cmkbr5_gene,_non-functional_mutant
y11999cds_31-358,mrna_for_inositol_1,4,5-trisphosphate_3-kinase/gb=y11999_/ntype=rna
- 20** z29090cds_2967-3183:in_reversesequence,_3201-3393,mrna_for_phosphatidylinositol_3-kinase
z69923cds_1572-1818:in_reversesequence,_6905-
7019,dna_sequence_from_cosmid_1219f9,_huntington's_dise
z84483cds_1166-1676,dna_sequence_from_pac_46h23,_brca2_gene_region_chromosome_13q12-
13_contains_klot
- 25** Metagene 218
- d89377_1587-2148,mrna_for_msx-2,_complete_cds,mrna_for_msx-2,_complete_cds
l01042_2723-3209,hiv1_tata_element_modulatory_factor_mrna_sequence_from_chromosome_3_
30 l02932_1331-1829,peroxisome_proliferator_activates_receptor_mrna,_complete_cds_
l40636_3438-3822,(clone_fbk_iii_16)_protein_tyrosine_kinase_(net_ptk)_mrna,_complete_cds
l77571mrna_1738-2218,dgs-a_mrna,_3'_end_
m13207exon#2-4_6-288:in_reversesequence,_2583:not_in_gb_record,granulocyte-
macrophage_colony-stimula
- 35** all_m19159_3664-4193,placental_heat-stable_alkaline_phosphatase_(plap-1)_gene,_complete_cds
m20681mrna#2_3326-3842,glucose_transporter-like_protein-iii_(glut3),_complete_cds
m21934_at_m21934_m21934,not_in_gb_record,rearranged_and_truncated_ig_gamma_heavy_chain
disease(riv)

- m22005cds_49-367,interleukingene_clone_pattacil-2c/2tt_complete_cds_clone_pattacil-2c/2tt/gb=m220
- m28210_356-686,gtp-binding_protein_(rab3a)_mrna_complete_cds_
- m30894_1015-1513,t-cell_receptor_ti_rearranged_gamma-chain_mrna_v-j-c_region_complete_cds_
- 5** m62800mrna_1350-1827,52-kd_ss-a/ro_autoantigen_mrna_complete_cds
- u28833_1571-2075,down_syndrome_critical_region_protein_(dscr1)_mrna_complete_cds
- u47292exon_120-564,spasmodytic_polypeptide_(sp)_gene_5'_region_and
- u64675_1439-1853,sperm_membrane_protein_bs-63_mrna_complete_cds_
- u66838_1138-1594,cyclin_a1_mrna_complete_cds
- 10** u67614_at_u67614_u67614,not_in_gb_record,sinusoidal_reduced_glutathione_transporter-associated_prote
- all_x54457_2328-2416,mrna_for_bile-salt-stimulated_lipase_(bssl)(ec_3.1.1.3)
- all_x59656_1286-1827,crk-like_gene_crkl
- all_x76342_1484-2019,adh7_mrna_
- 15** all_x78926_1271-1812,hzf3_mrna_for_zinc_finger_protein_
- x79568cds_1038-1314:in_reversesequence_1399-1627,bdp1_mrna_for_protein-tyrosine-phosphatase_
- all_y00787_1314-1469,mrna_for_mdncf(monocyte-derived_neutrophil_chemotactic_factor)_
- all_z29074_1968-2269,mrna_for_cytokeratin_9
- 20**
- Metagene 377
- d49488_640-1138,mrna_for_alpha-tocopherol_transfer_protein_complete_cds_
- l34363cds_3540-3847:in_reversesequence_4791-4896,x-
- 25** linked_nuclear_protein_(xnp)_gene_complete_cds_
- l39064mrna_3922-4348,interleukinreceptor_(il9r)_gene_complete_cds
- m20218exon_15-249:not_in_gb_record,coagulation_factor_xi_gene_
- m26665_267-484,histatin(his2)_mrna_complete_cds,histatin(his2)_mrna_complete_cds
- m59499mrna#1_3549-3891,lipoprotein-associated_coagulation_inhibitor_(laci)_gene
- 30** m61176_1093-1549,brain-derived_neurotrophic_factor_(bdnf)_mrna_complete_cds_
- u02632_2711-3047,calcium-activated_potassium_channel_mrna_partial_cds_
- u27193_1872-2346,protein-tyrosine_phosphatase_mrna_complete_cds_
- Metagene 96
- 35**
- hg2668-hi2764_at_hg2668-hi2764_bradykinin_receptor_
- u58032_1007-
- 1322,myotubularin_related_protein(mtmr1)_gene_partial_cds/gb=u58032/_ntype=dna/_annot=c
- u89012_2087-2639,dentin_matrix_acidic_phosphoprotein(dmp1)_mrna_complete_cds

Metagene 63

- d55638_227-659,b-cell_pabl_(pseudoautosomal_boundary-
5 like_sequence)_mrna,_clone_bc4/gb=d55638_/ntype
d78261_1293-1433,icsat_transcription_factor_mrna,_partial_cds,_similar_to_mouse_pip/lisrf_(irf-4)_s
hg1437-ht1437_s_at_hg1437-ht1437_proto-oncogene_trk
hg2825-ht2949_at_hg2825-ht2949_ret_transforming_gene_
10 hg3570-ht3773_at_hg3570-ht3773_protein_phosphatase_inhibitor_homolog_
hg668-ht4793_at_hg668-ht4793_t-cell_factor_1,_a/b/c,_altsplice_1,_a
j04430mrna_794-1350,tartrate-resistant_acid_phosphatase_typemrna,_complete_cds
l08187_551-1079,cytokine_receptor_(ebi3)_mrna,_complete_cds
l34059_2447-3017,cadherin-4_mrna,_complete_cds
15 m37984mrna_97-589,slow_twitch_skeletal_muscle/cardiac_muscle_troponin_c_gene,_complete_cds
m57506mrna_25-481,_scya1_gene_(secreted_protein_i-309)_extracted_fromsecreted_protein_(i-309)_gene_
m74089_1911-2271,tb1_gene_mrna,_3'_end_
s77094_1075-
20 1621,_nicotinic_acetylcholine_receptor_alpha_subunit|achr_alpha_subunit_[human,_thymic_c
s80050mrna_653-1133,_udp-n-acetylglucosamine:_alpha-6-d-mannoside_beta-1,6-n-
acetylglucosaminyltrans
s82185_419-905,_brag-1=brain-related_apoptosis_gene/bcl-2_homolog_[human,_mg-
107_glioma,_mrna_partia
25 u00928_611-1151,clone_ce29_4.1_(cac)n/(gtg)n_repeat-containing_mrna
u09412_1619-2045,zinc_finger_protein_znf134_mrna,_complete_cds_
u11878_4-169,interleukin-
8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb10,_partial_cds/gb=u118
u12775exon_156-342:not_in_gb_record,agouti_gene
30 u13022_1572-2124,negative_regulator_of_programmed_cell_death_ich-1s_(ich-
1)_mrna,_complete_cds_
u15306_3076-3466,cysteine-rich_sequence-specific_dna-
binding_protein_nfx1_mrna,_complete_cds_
u18259_6077-6647,clone_ciita-8_mhc_ii_transactivator_ciita_mrna,_complete_cds
35 u22178_3-321,prostatic_secretory_protein_57_mrna,_complete_cds/gb=u22178_/ntype=rna
u28488_1344-1847,putative_g_protein-coupled_receptor_(az3b)_mrna,_complete_cds_
u34877_511-997,biliverdin-ixalpha_reductase_mrna,_complete_cds_
u43959_758-815,betaadducin_mrna,_alternatively_spliced_partial_cds
u77129_2447-2975,sps1/ste20_homolog_khs1_mrna,_complete_cds

- u79247_1157-1559,clone_23599_mrna_sequence_
u83115_6327-6753,non-lens_beta_gamma-crystallin_like_protein_(aim1)_mrna,_partial_cds
u85430_3114-3279,transcription_factor_nfata4_mrna,_complete_cds
x04327mrna_1084-1564,erythrocyte_2,3-bisphosphoglycerate_mutase_mrna_ec_2.7.5.4
5 all_x13255_2280-2725,mrna_for_dopamine_beta-hydroxylase_type_a_(ec_1.14.17.1)
x15393mrna_19-541,motilin_gene_exon(and_joined_cds)
x59711cds_626-998:in_reversesequence,_1244-1280,mrna_for_caat-
box_dna_binding_protein_subunit_a_
x67337_2825-3365,hpbrii-4_mrna_
10 all_x69636_1268-1951,mrna_sequence_(15q11-13)
all_x78933_1420-1970,hzf10_mrna_for_zinc_finger_protein
x83441mrna_2724-3102,mrna_for_dna_ligase_iv
all_x90568_81371-81864,mrna_for_titin_protein_(clone_hh1-hh54)_
all_x91868_915-1378,mrna_for_six1_protein
15 all_x96754_846-1051,gene_encoding_kappa_light_chain_constant_region
x98206mrna_55-277:in_reversesequence,_307,mrna_for_uv-
b_repressed_sequence,_hur/gb=x98206_/ntype=rna

Metagene 77
20
u12767_4598-4922,mitogen_induced_nuclear_orphan_receptor_(minor)_mrna,_complete_cds
u79298_928-1312,clone_23803_mrna,_partial_cds
x58987mrna_1801-2299,mrna_for_d-1_dopamine_receptor
all_x97671_31-566,mrna_for_erythropoietin_receptor_
25
Metagene 380

m27281_642-1116,vascular_permeability_factor_mrna,_complete_cds
m75110_814-1312,h,k-atpase_beta_subunit_mrna,_complete_cds_
30 m99487_2039-2555,prostate-specific_membrane_antigen_(psm)_mrna,_complete_cds_
u73704_1248-1764,48_kda_fkbp-associated_protein_fap48_mrna,_complete_cds

Metagene 229

35 m27160mrna_1441-1879,tyrosinase_(tyr)_mrna,_complete_cds_
m64590_3317-3737,glycine_decarboxylase_mrna,_complete_cds
u26712_2910-3318,cbl-b_truncated_formlacking_leucine_zipper_mrna,_complete_cds

Metagene 345

d00632_1032-1470,plasma_(extracellular)_mrna_for_glutathione_peroxidase,_complete_cds
 d38145_1418-1952,mrna_for_prostacyclin_synthase,_complete_cds
 s77812_148-

- 5 211,flt=vascular_endothelial_growth_factor_receptor/vegf_receptor/cell_surface_tyrosine_
 u05861exon_50-243:not_in_gb_record,hepatic_dihydrodiol_dehydrogenase_gene_

Metagene 327

- 10 hg4167-ht4437_at_hg4167-ht4437_nuclear_factor_1,_a_type
 hg855-ht855_s_at_hg855-ht855_dna_excision_repair_protein_erc6_
 j05037_918-1368,serine_dehydratase_mrna,_complete_cds
 j05401_1158-1554,sarcomeric_mitochondrial_creatine_kinase_(mtck)_gene,_complete_cds
 l46353mrna_6579-7077,high-mobility_group_phosphoprotein_(hmgic)_gene,_exons_3-jan
 15 u10886_4762-5068,density_enhanced_phosphatase-1_mrna,_complete_cds_
 u22233_1659-2166,methylthioadenosine_phosphorylase_(mtap)_mrna,_complete_cds_
 all_x03350_1973-2514,mrna_for_alcohol_dehydrogenase_beta-1-subunit_(adh1-2_allele)_
 z94753exon_92-444:in_fullsequence,_1246-
 1265,dna_sequence_from_pac_465g10_on_chromosome_x_contains_m

20

Metagene 187

- 108835mrna#1_3166-
 3367_dm_kinase_gene_(myotonic_dystrophy_kinase)_extracted_frommyotonic_dystrophy_
 25 all_m19311_876-1059,calmodulin_mrna,_complete_cds,calmodulin_mrna,_complete_cds_
 u53506_1344-1836,type_ii_iodothyronine_deiodinase_mrna,_complete_cds.

Metagene 490

- 30 af005775_275-755,caspase-
 like_apoptosis_regulatory_protein(clarp)_mrna,_alternatively_spliced,_compl
 l35269exon_1602-2040,zinc_finger_protein_35_(znf35)_gene
 u32499_848-929,d3_dopamine_receptor_mrna,_complete_cds.
 u78107_667-1105,gamma_snap_mrna,_complete_cds
 35 u85946_2030-2288,brain_secretory_protein_hsec10p_(hsec10)_mrna,_complete_cds_

Metagene 484

ab003177_604-1096,mrna_for_proteasome_subunit_p27,_complete_cds

- hg3187-ht3366_s_at_hg3187-ht3366_tyrosine_phosphatase_1_non-receptor_altsplice_3_hg3546-ht3744_s_at_hg3546-ht3744_pre-mrna_splicing_factor_sf2p33_altsplice_form_1_m19650_1446-1700,2',3'-cyclic_nucleotide_3'-phosphodiesterase_mrna_complete_cds_s62904_2130-
- 5** 2523_thiopurine_methyltransferase [human_t84_colon_carcinoma_cell_mrna_2742_nt]_u47007_1818-2250,transcriptional_repressor_(nab1)_nab1_mrna_complete_cds_u51004_166-508,putative_protein_kinase_c_inhibitor_(pkci-1)_mrna_complete_cds_u90304_1272-1782,iroquois-class_homeodomain_protein_irx-2a_mrna_complete_cds_z93784cds_702-
- 10** 1008:in_reversesequence_58791:not_in_gb_record,dna_sequence_from_pac_398c22_on_chromo
- Metagene 480
- d38500_574-958,pms6_mrna_(yeast_mismatch_repair_gene_pms1_homologue)_partial_cds_(c-terminal_region
- 15** hg1751-ht1768_s_at_hg1751-ht1768_chorionic_somatotrophin_hormone_cs-5_hg1783-ht1803_s_at_hg1783-ht1803_islet_amyloid_polypeptide_hg4116-ht4386_s_at_hg4116-ht4386_olfactory_receptor_or17-219_114813_856-1147,carboxyl_ester_lipase_like_protein_(cell)_mrna_complete_cds_
- 20** 176703mrna_2687-3245,b56epsilon_mrna_complete_cds_m26856cds_1126-1456:in_reversesequence_3467-3600,21-hydroxylase_b_gene_complete_cds_all_m60746_531-844,histone_h3.1_(h1f3)_gene_complete_cds_s52028_582-1141,cystathionine_gamma-lyase_{clone_hcl-1}_{human_liver_mrna_1194_nt}s68271_891-1191,crem=cyclic_amp-responsive_element_modulator[human_mrna_1431_nt]
- 25** u03886_2214-2730,gs2_mrna_complete_cds_u10685exon#2_992-1142:in_reversesequence_3043-3271,mage-10_antigen_(mage10)_gene_complete_cds_u47050_2888-3296,putative_calcium_influx_channel_(htrp3)_mrna_complete_cds_u49114_2196-2700,prohormone_convertaseprecursor_(pc5)_mrna_partial_cds_
- 30** u58522_1608-2124,huntingtin_interacting_protein_(hip2)_mrna_complete_cds_u66036_732-1236,sulfotransferase_mrna_complete_cds_u74382_1317-1900,telomeric_repeat_dna-binding_protein_(pin2)_mrna_complete_cds_u84573_2882-3422,lysyl_hydroxylase_isoform(plod2)_mrna_complete_cds_u87593_f_at_u87593_u87593_4040_in_u87593_31-
- 35** 568,endogenous_retrovirus_clone_p1.8_polymerase_mrna_p_all_x16546_724-1319,dna_for_eosinophil_derived_neurotoxin_x17576cds_802-1078:in_reversesequence_1233-1389,melanoma_mrna_for_nck_protein_showing_homology_to_all_z22970_4355-4674,mrna_for_m130_antigen_cytoplasmic_variant_2_

Metagene 477

- ab000897_43-373,mrna_for_cadherin_fib3,_partial_cds/gb=ab000897_/ntype=rna
- 5** hg3033-ht3194_at_hg3033-ht3194_spliceosomal_protein_sap_62_
hg3426-ht3610_s_at_hg3426-ht3610_zinc_finger_protein_hzf-16,_kruppel-like,_altsplice_1_
l24559_1634-2078,dna_polymerase_alpha_mrna,_complete_cds
u07139_2039-2459,voltage-gated_calcium_channel_beta_subunit_mrna,_complete_cds_
u36500_2741-3209,lymphoid-specific_sp100_homolog_(lysp100-b)_mrna,_complete_cds
- 10** u46767_288-768,monocyte_chemoattractant_protein-4_precursor_(mcp-4)_mrna,_complete_cds_
all_u60269_13-524,endogenous_retrovirus_herv-
k(hml6)_proviral_clone_hml6.17_putative_polymerase_and_
x76223exon_2-540,mal_gene_exon_4.
x89267exon#10_225-
- 15** 312,dna_for_uroporphyrinogen_decarboxylase_gene/gb=x89267_/ntype=dna_/annot=exon_
x90978_1187-1751,mrna_for_an_acute_myeloid_leukaemia_protein_(1793bp)

Metagene 467

- 20** d38502_850-1120,pms4_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-
terminal_regio
d84145_458-980,ws-3_mrna,_complete_cds_
hg1828-ht1857_at_hg1828-ht1857_nexin,_glia-derived_
hg3513-ht3707_at_hg3513-ht3707_myosin,_heavy_polypeptide,_light_meromyosin_
25 hg3954-ht4224_s_at_hg3954-ht4224_landsteiner-wiener_blood_group_glycoprotein_(lw)
hg4114-ht4384_at_hg4114-ht4384_olfactory_receptor_or17-209_
reverse_j04742_384-607:in_j04742cds_49-110,autonomous_replicating_sequence_h1_(arsh1)_
l03785_72-582,regulatory_myosin_light_chain_(myl5)_mrna,_complete_cds
all_l26336_2691-3220,heat_shock_protein_hspa2_gene,_complete_cds_
30 l35253_972-1047,p38_mitogen_activated_protein_(map)_kinase_mrna,_complete_cds
l40388mrna_195-
675,thyroid_receptor_interactor_(trip15)_mrna,_5'_end_of_cds/gb=l40388_/ntype=rna
all_m21388_2-95,unproductively_rearranged_ig_mu-chain_mrna_v-region_(vd),_5'_end,_clone_mu-
3a1a.,unp
35 m21984_441-951,(clone_pwhnt16)_skeletal_muscle_troponin_t_mrna,_complete_cds
m31523_4155-4353,transcription_factor_(e2a)_mrna,_complete_cds_
m33653_467-965,(clones_ht-[125,133])_alpha-2_type_iv_collagen_(col4a2)_mrna,_complete_cds
m62840mrna_1755-2175,acyloxyacyl_hydrolase_mrna,_complete_cds
m65134mrna_3588-4102,complement_component_c5_mrna,_3'_end

- m90391_1736-2866,putative_il-16_protein_precursor, mrna, complete_cds
s66427_4218-4764,rbp1=retinoblastoma_binding_protein[human,nalm-6_pre-
b_cell_leukemia, mrna, 4834_
s70609_1781-2339, glycine_transporter_type_1b [human, substantia_nigra, mrna, 2364_nt]
5 s81264_50-243,hs-tbx2=t-box_gene_{t-
box_region}_[human,fetal_kidney, mrna_partial, 283_nt]/gb=s812
u03486cds_625-1045:in_reversesequence, 1121-1211,connexin40_gene, complete_cds
u06632_2039-2579,p80-coilin_mrna, complete_cds_
u16997_1218-1764,orphan_receptor_ror_gamma_mrna, complete_cds
10 u19487_1843-2329,prostaglandin_e2_receptor_mrna, complete_cds
u21936_2630-3038,peptide_transporter_(hpept1)_mrna, complete_cds_
u27459_2534-2984,origin_recognition_complex_protein homolog_horc21_mrna, complete_cds
u43318_1805-2291,putative_transmembrane_receptor_(frizzled_5)_mrna, complete_cds_
u51010exon_17-222,nicotinamide_n-
15 methyltransferase_gene, exonand_5'_flanking_region/gb=u51010_/ntype
u59289_3350-3824,h-cadherin_mrna, complete_cds_
u61374_1265-
1715,novel_protein_with_short_consensus_repeats_of_six_cysteines_mrna, complete_cds
u61836mrna_540-972,putative_cyclin_g1_interacting_protein_mrna, partial_sequence_
20 u62317mrna#7_2016-
2532_hypothetical_protein_384d8gene_extracted_from_chromosome_22q13_bac_clone_cit
u66617_2252-
2786,swi/snf_complex_60_kda_subunit_(baf60a)_mrna, alternatively_spliced, complete_cds_
u78027mrna#4_1964-2372, 1441_gene_(144-
25 like_ribosomal_protein)_extracted_frombruton_tyrosine_kinase_
u82256_1325-1823,arginase_type_ii_mrna, complete_cds_
u82303_25-313,unknown_protein_mrna, partial_cds/gb=u82303_/ntype=rna_
u95020_1276-1786,voltage-dependent_calcium_channel_beta-4_subunit_mrna, complete_cds.
x04898mrna_49-445, gene_for_apolipoprotein_a_ii_
30 all_x52056_778-1304, mrna_for_spi-1_proto-oncogene
x59770mrna_685-1213,il-1r2_mrna_for_type_ii_interleukin-1_receptor_(cell_line_cb23)_
x61177mrna_1495-1933,hsil5r2_gene_for_interleukin-5_receptor_type_2
x79780cds_94-622:in_reversesequence, 646,ypt3_mrna
all_z35085_1960-2506, mrna_for_unknown_antigen
35 z47055cds_437-968,partial_cdna_sequence, farnesyl_pyrophosphate_synthetase_like-
4/gb=z47055_/ntype=d

Metagene 459

- d21853_1111-1543,mrna_for_kiaa0111_gene_complete_cds
- d79986_4973-5513,mrna_for_kiaa0164_gene_complete_cds
- d87077_5465-5975,mrna_for_kiaa0240_gene_partial_cds_
- hg3076-ht3238_s_at_hg3076-ht3238_heterogeneous_nuclear_ribonucleoprotein_k_altsplice_1
- 5 hg3514-ht3708_at_hg3514-ht3708_tropomyosin_tm30nm_cytoskeletal
- hg4322-ht4592_at_hg4322-ht4592_tubulin_beta_
- j02621mrna_653-1214,non-histone_chromosomal_protein_hmg-14_mrna_complete_cds
- j04029_1450-2007,keratintype_i_intermediate_filament_(krt10)_mrna_complete_cds_
- j04152mrna_1181-1648_mls1_gene_extracted_fromgastrointestinal_tumor-
- 10 associated_antigen_ga733-1_prot
- l37368_1849-2359,(clone_e5.1)_rna-binding_protein_mrna_complete_cds_
- l40397mrna_979-1267,(clone_s31i125)_mrna_3'_end_of_cds_
- l42379mrna_2645-3155,bone-derived_growth_factor_(bpgf-1)_mrna_complete_cds_
- ml6342mrna#2_1287-
- 15 1581,nuclear_ribonucleoprotein_particle_(hnmp)_c_protein_mrna_complete_cds_
- m19311mrna_520-1052,calmodulin_mrna_complete_cds,calmodulin_mrna_complete_cds_
- m23379_3723-4179,gtpase-activating_protein_ras_p21_(rasa)_mrna_complete_cds_
- u00947_1301-1347,clone_c4e_3.2_(cac)n/(gtg)n_repeat-containing_mrna
- u06631_3269-3779,(h326)_mrna_complete_cds_
- 20 u20998_973-1417,signal_recognition_particle_subunit(srp9)_mrna_complete_cds_
- u35048_1159-1675,tsc-22_protein_mrna_complete_cds_
- u35451_1643-2027,heterochromatin_protein_p25_mrna_complete_cds
- u57877_766-1144,integral_membrane_protein_cii-
- 3_mrna_nuclear_gene_encoding_mitochondrial_protein_c
- 25 u77948_2714-3236,bruton_tyrosine_kinase-associated_protein-135_mrna_complete_cds
- u79282_1087-1651,clone_23801_mrna_sequence_
- u90549_1452-1932,non-histone_chromosomal_protein_(nhc)_mrna_complete_cds
- u90551_1071-1623,histone_2a-like_protein_(h2a/l)_mrna_complete_cds
- u95740mrna#1_5316-
- 30 5856_362g6.1_gene_(unknown_protein_cit987sk_362g6_1)_extracted_fromchromosome_16p
- x01703exon#4_929-1151,gene_for_alpha-tubulin_(b_alpha_1)_
- x15729cds_1538-1820:in_reversesequence_2069-2215,mrna_for_nuclear_p68_protein
- x59405exon#12_1560-2040_h_sapiens_gene_for_membrane_cofactor_protein
- all_x63753_5116-5621,son-a_mrna
- 35 all_x68194_1513-2090,h-sp1_mrna
- all_x72841_1378-1937,ief_7442_mrna_
- all_x74104_650-1059,mrna_for_trap_beta_subunit_
- all_x75304_9705-10252,giantin_mrna_
- x81003mrna_1032-1560,hcg_v_mrna

all_x81198_3084-3673,mrna_(clone_p5)_for_archain_
 all_x81625_3058-3617,mrna_for_cl1_protein
 all_x84908_3722-3975,mrna_for_phosphorylase-kinase,_beta_subunit_
 all_x86098_2367-2704,mrna_for_bs69_protein_
5 all_x95648_1063-1658,mrna_for_eif-2b_alpha_subunit_
 all_z72499_3157-3740,mrna_for_herpesvirus_associated_ubiquitin-specific_protease_(hausp).

Metagene 446

- 10** d17391_2957-3497,mrna_for_alpha_4(iv)_collagen,_c-terminal_
 hg4582-ht4987_at_hg4582-ht4987_glucocorticoid_receptor,_beta_
 104569_8323-8890,(clone_hht-1)_1-type_voltage-
 dependent_calcium_channel_a1_subunit_(hht)_mrna,_compl
 m37815mrna#1_1079-1589,_cd28_gene_(glycoprotein_cd28)_extracted_from-
15 cell_membrane_glycoprotein_cd2
 z49995mrna_2014-2590,mrna_(non-coding;_clone_h2a)

Metagene 435

- 20** d14874_908-1406,mrna_for_adrenomedullin,_complete_cds
 d50857_5954-6440,dock180_protein_mrna,_complete_cds
 hg1428-ht1428_s_at_hg1428-ht1428_globin,_beta
 hg2815-ht2931_s_at_hg2815-ht2931_myosin,_light_chain,_alkali,_smooth_muscle,_non-
 muscle,_altsplice_2
25 hg3523-ht4899_s_at_hg3523-ht4899_proto-oncogene_c-myc,_altsplice_3,_orf_114
 l09235_1323-1845,vacuolar_atpase_(isoform_va68)_mrna,_complete_cds_
 l10838_79-499,sr_protein_family,_pre-mrna_splicing_factor_(srp20)_mrna,_complete_cds
 l42601cds_1334-1665:in_reversesequence,_247-470,keratinisoform_k6c_(krt6c)_gene_
 m81637_1078-1603,grancalcin_mrna,_complete_cds_
30 s82297_3-391,_beta_2-microglobulin_{11bp_deleted_between_nucleotides_98-
 99}_{human,_colon_cancer_cel
 u07158_641-1169,syntaxin_mrna,_complete_cds
 u37518_1162-1390,tnf-related_apoptosis_inducing_ligand_trail_mrna,_complete_cds
 u43083_1408-1582,g_alpha-q_(gaq)_mrna,_complete_cds
35 u84569_647-1217,yf5_mrna,_complete_cds_
 u91327mrna_156-654,chromosome_12p15_bac_clone_cit987sk-
 99d8_complete_sequence/gb=u91327/_ntype=dna_
 x03689cds_17-255,mrna_fragment_for_elongation_factor_tu_(n-terminus)/gb=x03689/_ntype=rna
 x89399_s_at_x89399_x89399,not_in_gb_record,mrna_for_ins(1,3,4,5)p4-binding_protein

x95073_657-1119,mrna_for_translin_associated_protein_x_

Metagene 404

- 5 d87009cds#5_1325-1565:in_fullsequence,_35519-
35735,_5'_oyl11.1_gene_extracted_from(lambda)_dna_for_im
m68895mrna_858-1278,alcohol_dehydrogenasegene,_complete_cds
x54489mrna_660-1034,gene_for_melanoma_growth_stimulatory_activity_(mgsa)
all_x68242_408-889,mrna_for_hin-1

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Metagene 338

- d50370_2047-2581,mrna_for_nucleosome_assembly_protein,_complete_cds
l43576_709-1009,(clone_est02946)_mrna_
15 m36118_491-828,cytotoxin_serine_protease-c_mrna,_complete_cds
s81419_25-
349,_dystrophin,_dystrophin_{purkinje_promoter,_alternatively_spliced}_{human,_cortical_br
u04735_1728-2184,microsomal_stress_70_protein_atpase_core_(stch)_mrna,_complete_cds
u45255mrna_1576-1952,paired-box_protein_pax2_(pax2)_gene_
20 u58331_762-1041,placental_delta_sarcoglycan_mrna,_complete_cds_
u63139_5305-5779,rad50_(rad50)_mrna,_complete_cds
x92110mrna_714-1242,mrna_for_hcgvihi protein_
z47553mrna_1761-2247,mrna_for_flavin-containing_monooxygenase(fmo5)_

25 Metagene 316

- hg172-ht3924_at_hg172-ht3924_spermidine/spermine_n1-acetyltransferase,_altsplice_2_
s79267_2828-3398,_cd4_receptor_{exonsand_2}_{human,_t-lymphocyte,_mrna,_3429_nt]
u10868_2267-2765,aldehyde_dehydrogenase_aldh7_mrna,_complete_cds_
30 u31449_773-1337,intestinal_and_liver_tetraspan_membrane_protein_(il-tmp)_mrna,_complete_cds
u57911_1693-2203,fetal_brain_(239fb)_mrna,_from_the_wagr_region,_complete_cds
u67934cds_375-501:in_reversesequence,_549-
765,44.9_kda_protein_c18b11_homolog_gene,_partial_cds
x58022mrna_803-1223,mrna_for_corticotropin-releasing_factor_binding_protein_(crf-bp)_

35

Metagene 299

s75881_234-719,_a-myb=dna-binding_transactivator_{3'_region}_{human,_ccrf-cem_t-
leukemia_line,_mrna_

z21707cds_552-912:in_reversesequence,_954-984,p18_mrna

Metagene 298

- 5 d64110_615-1161,mrna_for_tob_family,_complete_cds
hg2564-ht2660_s_at_hg2564-ht2660_gamma-aminobutyric_acid_(gaba)_a_receptor,_alpha_subunit
j04056_746-1118,carbonyl_reductase_mrna,_complete_cds
m64174_3012-3468,protein-tyrosine_kinase_(jak1)_mrna,_complete_cds_
u82319_470-980,clone_ydd19_mrna_sequence_
- 10 x67594cds_507-909:in_reversesequence,_1119-1221,mrna_for_msh_receptor_

Metagene 296

- m69177_1992-2436,monoamine_oxidase_b_(maob)_mrna,_complete_cds_
- 15 m94151_3127-3631,cadherin-associated_protein-related_(cap-r)_mrna,_complete_cds
u01102exon#1-3_4-
109:not_in_gb_record,lung_clara_cellskda_secretory_protein_(cc10)_gene,_satellite_a
u49835_832-1361,ykl-39_precursor_mrna,_complete_cds
u88898_561-757,endogenous_retroviral_h_protease/integrase-
20 derived_orf1_mrna,_complete_cds,_and_putat

Metagene 277

- ac000066cds_2985-3237:in_reversesequence,_48519-48663,bac_clone_rg293f11_from_7q21-7q22_
- 25 af000560_1220-1697,ttf-i_interacting_peptidemrna,_partial_cds.
d86958_6175-6430,mrna_for_kiaa0203_gene,_complete_cds
hg3369-ht3546_at_hg3369-ht3546_potassium_channel,_voltage-gated,_isk-
related_family,_member_1
l43575mrna_1021-1106,(clone_48a8)_mrna
- 30 m15841_492-945,u2_small_nuclear_rna-associated_b" _antigen_mrna,_complete_cds
m27878_2656-3172,dna_binding_protein_(hpf2)_mrna,_complete_cds_
m31516mrna_1492-2002,decay-accelerating_factor_mrna,_complete_cds
m34309_4410-4836,epidermal_growth_factor_receptor_(her3)_mrna,_complete_cds
m99436_1808-2246,transducin-like_enhancer_protein_(tle2)_mrna,_complete_cds
- 35 u18242_761-1265,calcium_modulating_cyclophilin_ligand_(camlg)_mrna,_complete_cds_
u51334_1840-2068,putative_rna_binding_protein_(rbp56)_mrna,_complete_cds_
u60205_1192-1726,methyl_sterol_oxidase_(erg25)_mrna,_complete_cds
u65928_711-1125,jun_activation_domain_binding_protein_mrna,_complete_cds_
u82279_1505-2069,immunoglobulin-like_transcriptmma,_complete_cds_

- u91521_2098-2470,peroxin(hspex12)_mrna,_complete_cds.
 all_x79353_1624-2189,xap-4_mrna_for_gdp-dissociation_inhibitor_
 all_x80754_1279-1862,mrna_for_gtp-binding_protein
 x81851cds_26-326,_hsapiens_il-4_gene_splice_variant/gb=x81851_/ntype=ma
5 all_x83543_7066-7427,apxl_mrna_
 x90999cds_390-726:in_reversesequence,_828-942,mrna_for_glyoxalase_ii
 all_x99584_197-630,mrna_for_smt3a_protein
 all_y00291_2443-2888,hap_mrna_encoding_a_dna-binding_hormone_receptor
 all_y07566_951-1066,mrna_for_rit_protein_
10
 Metagene 270
 d45917_634-1120,mrna_for_timp-3,_partial_cds_(c-terminus_region)_
 d83174_1524-1896,mrna_for_collagen_binding_protein_2,_complete_cds_
15 d86479_2250-2814,mrna_for_aebp1_gene,_complete_cds_
 d87258_1489-1999,cancellous_bone_osteoblast_mrna_for_serin_protease_with_igf-
 binding_motif,_complete
 hg2197-ht2267_s_at_hg2197-ht2267_collage,_type_vii,_alpha_1
 hg3543-ht3739_at_hg3543-ht3739_insulin-like_growth_factor_
20 hg987-ht987_at_hg987-ht987_mac25_
 j02611mrna_208-766,apolipoprotein_d_mrna,_complete_cds_
 j03040_1508-2000,sparc/osteonectin_mrna,_complete_cds
 j03278_5029-5485,platelet-derived_growth_factor_(pdgf)_receptor_mrna,_complete_cds_
 l32137_1910-2309,germline_oligomeric_matrix_protein_(comp)_mrna,_complete_cds
25 l36033_2929-3343,pre-b_cell_stimulating_factor_homologue_(sdf1b)_mrna,_complete_cds
 m11718_716-1274,alpha-2_type_v_collagen_gene,_3'_end_
 m16279mrna_757-1153,mic2_mrna,_complete_cds
 m25269_1791-2211,tyrosine_kinase_(elk1)_oncogene_mrna,_complete_cds_
 m55593mrna#1_2600-2936,collagenase_type_iv_(clg4)_gene_
30 m85289_14032-14302,heparan_sulfate_proteoglycan_(hspg2)_mrna,_complete_cds_
 m96233exon#8_114-467,glutathione_transferase_mu_number(gstm4)_gene,_complete_cds
 all_u14394_4004-4533,tissue_inhibitor_of_metalloproteinases-3_mrna,_complete_cds_
 u16306_10722-11142,chondroitin_sulfate_proteoglycan_versican_v0_splice-
 variant_precursor_peptide_mrn
35 u24389cds_1495-1696:in_reversesequence,_207-339:not_in_gb_record,lysyl_oxidase-
 like_protein_gene_
 u60115_1863-2211,skeletal_muscle_lim-protein_slim1_mrna,_complete_cds
 u77846mrna_979-
 l356,elastin_gene,_partial_cds_and_partial_3'_utr,elastin_gene,_partial_cds_and_parti

all_x15880_1690-2273,mrna_for_collagen_vi_alpha-1_c-terminal_globular_domain_
 x15882cds_984-1230:in_reversesequence,_1272-1554,mrna_for_collagen_vi_alpha-2_c-
 terminal_globular_do
 x79683cds_4908-5361:in_reversesequence,_5594-5620,lamb2_mrna_for_beta2_laminin
5 x86693mrna_2171-2675,mrna_for_hevin_like_protein_
 z48199exon#4_1510-2026,syndecan-1_gene_(exons_2-5)_
 z49269exon#1-3_76-199:not_in_gb_record,gene_for_chemokine_hcc-1_

Metagene 265

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d84110_1113-1515,mrna_for_werner_syndrome-1/type_4,_complete_cds_
 d86982_5824-6286,mrna_for_kiaa0229_gene,_partial_cds_
 hg4518-ht4921_at_hg4518-ht4921_transcription_factor_btf3_homolog_
 x04085mrna_1684-
15 2236,gene_for_catalase_(ec_1.11.1.6)_5' flank_and_exonmapping_to_chromosome_11,_band
 x67098exon#8_40-454,rts_alpha_mrna_containing_four_open_reading_frames_

Metagene 247

20

d86983_5131-5485,mrna_for_kiaa0230_gene,_partial_cds_
 hg142-ht142_at_hg142-ht142_modulator_recognition_factor_
 hg3995-ht4265_at_hg3995-ht4265_cpg-enriched_dna,_clone_s19_
 j04599_1078-1630,hpgi_mrna_encoding_bone_small_proteoglycan_i_(biglycan),_complete_cds_
 j05243_7216-7732,nonerythroid_alpha-spectrin_(sptan1)_mrna,_complete_cds_

25

l06139_3573-4083,receptor_protein-tyrosine_kinase_(tek)_mrna,_complete_cds
 l41143_1635-2085,expressed_pseudo_tcta_mrna_at_t(1;3)_translocation_site,_complete_cds
 m13194mrna_586-1006,excision_repair_protein_(ercc1)_mrna,_complete_cds,_clone_pcde_
 m25079_163-230,sickle_cell_beta-globin_mrna,_complete_cds
 m57609mrna_4490-5012,dna-binding_protein_(gli3)_mrna,_complete_cds_

30

x15306mrna_3269-3707,nf-h_gene,_exon(and_joined_cds)_
 x75546cds_626-926:in_reversesequence,_1204,mrna_for_fibromodulin
 z83799_15-239,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc1).
 all_z84721_30317-
 34635,dna_sequence_from_cosmid_gg1_from_a_contig_from_the_tip_of_the_short_arm_of_c

35

Metagene 243

m60974_731-1304,growth_arrest_and_dna-damage-
 inducible_protein_(gadd45)_mrna,_complete_cds_

all_x14894_826-1385,mrna_for_myogenic_factor_myf-5_

Metagene 242

- 5** d10704_1969-2365,mrna_for_choline_kinase_
d13413mrna_578-617,mrna_for_tumor-
associated_120_kda_nuclear_protein_p120,_partial_cds(carboxyl_term
d13900_748-1234,mrna_for_mitochondrial_short-chain_acyl-coa_hydratase,_complete_cds_
d64108_1595-2079,mrna_for_dmc1_homologue,_complete_cds_
10 hg3999-ht4269_at_hg3999-ht4269_retinoic_acid_receptor,_beta_isoform_1_
j03071cds#3_151-604:in_reversesequence,_14327-28953,_growth_hormone_gh-
1_gene_extracted_fromgrowth_h
l13042exon#2-3_11-216:not_in_gb_record,calbindin_d-9k_gene,_5'_end_cds_
l14778_1665-2225,calmodulin-
15 dependent_protein_phosphatase_catalytic_subunit(ppp3ca)_mrna,_complete_
l37043mrna_742-1294,casein_kinase_i_epsilon_mrna,_complete_cds
l46720cds_2231-2557:in_reversesequence,_2650-2828,autotaxin-t(atx-t)_gene,_complete_cds
all_m55420_605-897:in_m55420cds_109-140,ige_chain,_lastexons_
m63904mrna_1519-2029,g-alphaprotein_mrna,_complete_cds_
20 m65066_1903-2323,camp-dependent_protein_kinase_regulatory_subunit_ri-beta_mrna,_3'_end_
m75099_25-493,rapamycin_and_fk506-binding_protein,_complete_cds_
m87338_1120-1660,replication_factor_40-kda_subunit(al)_mrna,_complete_cds
s68616_4005-4491,_na⁺/h⁺_exchanger_nhe-1_isoform_[human,heart,mrna,4516_nt]
u20530_47-593,bone_phosphoprotein_spp-
25 24_precursor_mrna,_complete_cds/gb=u20530_/ntype=rna_
u22398_1030-1468,cdk-inhibitor_p57kip2(kip2)_mrna,_complete_cds_
u33839_at_u33839_u33839,not_in_gb_record,potassium_channel_mrna,_complete_cds/gb=u33839_
/ntype=rna
u61262_4667-5195,neogenin_mrna,_complete_cds_
30 u66619_1165-1699,swi/snf_complex_60_kda_subunit(baf60c)_mrna,_complete_cds
u82313_133-439,unknown_protein_mrna,_partial_cds/gb=u82313_/ntype=rna
x69391cds_395-821,mrna_for_ribosomal_protein_l6
all_x82693_134-681,mrna_for_e48_antigen

35 Metagene 241

d83735_1551-2085,adult_heart_mrna_for_neutral_calponin,_complete_cds_
j04182_1914-2394,lysosomal_membrane_glycoprotein-1(lamp1)_mrna,_complete_cds_
all_108895_3518-4059,mads/mef2-family_transcription_factor(mef2c)_mrna,_complete_cds_

- m19267_1476-1600,tropomyosin_mrna,_complete_cds
 all_m19481_278-651:in_m19481cds_818-921,follistatin_gene
 m21574mrna_5807-6293,platelet-
 derived_growth_factor_receptor_alpha_(pdgfra)_mrna,_complete_cds_
- 5** m74719_1971-2475,sef2-1b_protein_(sef2-1b)_mrna,_complete_cds
 m95787_494-1004,22kda_smooth_muscle_protein_(sm22)_mrna,_complete_cds
 s57132_3108-
 3615_coll16a1=type_xvi_collagen_alphachain_[human,placenta,mrna_partial,3720_nt]
 s73591_2169-2649,brain-expressed_hhcap78_homolog_[human,hl-
- 10** 60_acute_promyelocytic_leukemia_cells,_
 u26710_3398-3878,cbl-b_mrna,_complete_cds
 u44975_791-1301,dna-binding_protein_cpbp_(cpbp)_mrna,_partial_cds
 u53446_2680-3220,mitogen-responsive_phosphoprotein_doc-2_mrna,_complete_cds
 u82532_231-753,gdi-dissociation_inhibitor_rhogdigamma_mrna,_complete_cds
- 15** u90913_659-1157,clone_23665_mrna_sequence
 all_x13839_768-1300,mrna_for_vascular_smooth_muscle_alpha-actin
 all_x86809_1916-2367,mrna_for_major_astrocytic_phosphoprotein_pea-15_
 y12670mrna_531-1011,ob-rgrp_gene/gb=y12670_/ntype=rna
 all_z24727_1355-1569,tropomyosin_isoform_mrna,_complete_cds
- 20** z26248cds_178-640:in_reversesequence,_1512,mrna_for_eosinophil_granule_major_basic_protein
 all_z48923_3300-3835,mrna_for_bmpr-ii
- Metagene 240
- 25** hg491-ht491_at_hg491-ht491_fc_receptor_iib3_for_igg,_low_affinity
 m73720mrna_1032-1584,mast_cell_carboxypeptidase_a_(mc-cpa)_gene
 m82919_1201-1579,gamma_amino_butyric_acid_(gabaa)_receptor_beta-
 3_subunit_mrna,_complete_cds_
 u27109_3633-4155,prepromultimerin_mrna,_complete_cds_
- 30** Metagene 203
- d50582cds_954-1128:in_reversesequence,_1367-
 1535,gene_for_inward_rectifier_k_channel,_complete_cds_
- 35** hg2365-ht2461_at_hg2365-ht2461_glyceraldehyde-3-phosphate_dehydrogenase
 hg4188-ht4458_at_hg4188-ht4458_n-methyl-d-aspartate_receptor_subunit,_splice_variant_hnr1n_
 j00146_388-718,dihydrofolate_reductase_pseudogene_(psi-hd1)
 l23808_1297-1717,metalloproteinase_(hme)_mrna,_complete_cds
 l27071_1963-2527,tyrosine_kinase_(tkk)_mrna,_complete_cds

- l37378mrna_3182-3680,guanylyl_cyclase_(retgc-2)_mrna,_complete_cds
 l40380mrna_285-795,thyroid_receptor_interactor_(trip11)_mrna,_3'_end_of_cds_
 all_l48728_380-
 657:not_in_gb_record,_tcrbv10s1_gene_extracted_fromt_cell_receptor_beta_(tcrbv10s1)_g
5 m18079cds_85-343:in_reversesequence,_4158-
 4278,_human,_intestinal_fatty_acid_binding_protein_gene,_c
 m23234mrna_3313-3865,membrane_glycoprotein_p_(mdr3)_mrna,_complete_cds_
 m29386mrna_200-701,prolactin_mrna,_3'_end
 m94633exon_1275-
10 1611,recombination_acitivating_protein_(rag2)_gene,_last_exon/gb=m94633_/ntype=dna_
 s77763_1132-
 1624,_nuclear_factor_erythroidisoform_f=basic_leucine_zipper_protein_{alternatively_spli
 all_u07807_3319-4740:in_u07807cds_13-110,metallothionein_iv_(mtiv)_gene,_complete_cds_
 u10687exon#10_1056-1412,mage-4a_antigen_(mage4a)_gene,_complete_cds
15 u11690_3665-4241,faciogenital_dysplasia_(fgd1)_mrna,_complete_cds
 u13948_3283-3787,zinc_finger/leucine_zipper_protein_(af10)_mrna,_complete_cds
 u19345_2258-2756,arl_protein_(ar)_mrna,_complete_cds_
 u26174_499-991,pre-granzymemrna,_complete_cds_
 u33017_1248-1680,signaling_lymphocytic_activation_molecule_(slam)_mrna,_complete_cds_
20 u35459_629-1109,bomapin_mrna,_complete_cds/gb=u35459_/ntype=rna
 u52521_753-1131,arfaptin_1,_putative_target_protein_of_adp-
 ribosylation_factor,_mrna,_complete_cds_
 u72671_2390-2930,telencephalin_precursor_mrna,_complete_cds
 u96115_162-594,ww_domain-containing_protein_wwp3_mrna,_partial_cds/gb=u96115_/ntype=rna_
25 x12453mrna_993-1539,mrna_for_retinal_s-antigen_(48_kda_protein)
 all_x12530_1083-1415,mrna_for_b_lymphocyte_antigen_cd20_(b1,_bp35)_
 x17648cds#2_1069-1177:in_reversesequence,_1341-1605,mrna_for_granulocyte-
 macrophage_colony-stimulati
 all_x17651_829-1412,myf-4_mrna_for_myogenic_determination_factor_
30 all_x52520_2414-2673,mrna_for_tyrosine_aminotransferase_(tat)(ec_2.6.1.5)_
 x54131mrna_5534-6026,hptp_beta_mrna_for_protein_tyrosine_phosphatase_beta
 x57303cds_1488-1866:in_reversesequence,_2022-2028,rec11_mrna
 x61615cds_2830-3160:in_reversesequence,_3482-
 3548,mrna_for_leukemia_inhibitory_factor_(lif)_receptor
35 x65550exon#15_2051-2549,mki67a_mrna_(long_type)_for_antigen_of_monoclonal_antibody_ki-
 67_
 all_y10032_1065-1588,mrna_for_putative_serine/threonine_protein_kinase_
 all_z29067_1423-1802,nek3_mrna_for_protein_kinase
 z30425cds_649-1009:in_reversesequence,_1299-1311,mrna_for_orphan_nuclear_hormone_receptor.

z35491mrna_797-1253,mrna_for_novel_glucocorticoid_receptor-associated_protein

Metagene 199

- 5** ac002086cds_1686-1974:in_reversesequence,_98485,pac_clone_dj525n14_from_xq23
k03218cds_1068-1587:in_reversesequence,_197-230,c-src-1_proto-oncogene
117418exon_3-
229:not_in_gb_record,_complement_receptorgene_extracted_fromcomplement_receptor_type(al
126953_2282-2846,chromosomal_protein_mrna,_complete_cds_
10 u96136_4729-5233,delta-catenin_mrna,_complete_cds

Metagene 194

- 136642mrna_3940-4474,receptor_protein-tyrosine_kinase(hek11)_mrna,_complete_cds
15 178833cds#3_363-645:in_fullsequence,_17171-
17279,_brca1_gene_extracted_frombrca1_rho7_and_vati_gene
m81886_2390-2861,glutamate_receptor_type(hbgr1)_mrna,_complete_cds
all_u17579_1465-1982,_growth_hormone-
releasing_hormone_receptor_form_b_gene_extracted_fromgrowth_hor

20

Metagene 193

- d78334_496-1018,mrna_for_ankyrin_motif,_complete_cds_
u59228_407-797,ectodermal_dysplasia_protein(eda)_mrna,_complete_cds_
25 x07384cds_2933-3269:in_reversesequence,_3377-3527,mrna_for_gli_protein
all_x73608_2895-3478,mrna_for_testican_

Metagene 189

- 30** af000562_43-427,uroplakin_ii_mrna,_partial_cds
d63134mrna_73-439,mrna_for_ets-like_30_kda_protein/gb=d63134_/ntype=rna
all_j00220_1704-1849,ig_germline_h-chain_g-e-a_region_a:_gamma-3_5'_flank,ig_germline_h-
chain_g-e-a_
all_j05253_8895-9496,interstitial_retinol-binding_protein(irbp)_gene,_complete_cds
35 l37792mrna_1565-2015,syntaxin_1a_mrna,_complete_cds
all_m23533_3030-3556,alphaadrenergic_receptor_gene,_complete_cds
m29610_179-451,glycophorin_e_mrna,_complete_cds,glycophorin_e_mrna,_complete_cds
u13706_3-63,elav-like_neuronal_proteinisoform_hel-n2_(hel-
n1)_mrna,_partial_cds/gb=u13706_/ntype=rna

- u14383_958-1372,mucin_(muc8)_mrna,_partial_cds_
u20536_935-1428,cysteine_protease_mch2_isoform_alpha_(mch2)_mrna,_complete_cds_
u33921_578-1046,_hsu33921cdna_
u50535_1856-2270,bra2_region,_mrna_sequence_cg006_
5 u58970_1284-
1824,putative_outer_mitochondrial_membrane_34_kda_translocase_htom34_mrna,_complete_cds
u66406_2835-3255,putative_eph-related_ptk_receptor_ligand_lerk-8_(eplg8)_mrna,_complete_cds
u90065_615-1178,potassium_channel_kcno1_mrna,_complete_cds_
v00551mrna_366-878,_messenger_rna_forleukocyte_(alpha)_interferon
10 all_x05345_1772-1953,mrna_for_histidyl-trna_synthetase_(hrs)_
x14448mrna_1017-1299:in_reversesequence,_11301-11319,gla_gene_for_alpha-d-
galactosidase_a_(ec_3.2.1.
x86012cds_61-319:in_fullsequence,_6603-
6795,dna_sequence_from_intron_22_of_the_factor_viii_gene,_xq2
15 all_y00477_5141-
5216,bone_marrow_serine_protease_gene_(medullasin)_(leukocyte_neutrophil_elastase_ge
Metagene 173
20 m24736_3222-3785,endothelial_leukocyte_adhesion_molecule(elam-1)_mrna,_complete_cds_
y07565cds_307-614:in_reversesequence,_833-1024,mrna_for_rin_protein_
Metagene 167
25 hg4704-ht5146_at_hg4704-ht5146_glial_growth_factor
m19301mrna_944-1448,branched-chain_alpha-
keto_acid_dehydrogenase_(e2)_mrna,_complete_cds_
m95610_1971-2493,alphanotype_ix_collagen_(col9a2)_mrna,_partial_cds_
u65437mrna_7-307,homeodomain-containing_protein_(hanf)_gene,_partial_cds_
30
Metagene 161
ab006781_528-1007,mrna_for_galectin-4,_complete_cds/gb=ab006781/_ntype=rna
af007111_1609-2017,mdm2-like_p53-binding_protein_(mdmx)_mrna,_complete_cds_
35 d49357_958-1438,mrna_for_s-adenosylmethionine_synthetase,_complete_cds_
d86984_5659-6139,mrna_for_kiaa0231_gene,_partial_cds_
hg2261-ht2351_s_at_hg2261-ht2351_antigen,_prostate_specific,_altsplice_form_2
hg3527-ht3721_f_at_hg3527-ht3721_luteinizing_hormone,_beta_subunit_
hg3994-ht4264_at_hg3994-ht4264_cpg-enriched_dna,_clone_s16_

- hg4058-ht4328_at hg4058-ht4328 oncogene aml1-evi-1, fusion activated_
 hg4533-ht4938_at hg4533-ht4938 kallistatin, protease inhibitor 4_
 j04739mrna_1212-1650,bactericidal permeability increasing protein (bpi) mrna, complete cds_
 115309_2444-2960,zinc_finger_protein (znf141) mrna, complete cds_
5 117075_1130-1607,tgf-b_superfamily_receptor_type_i mrna, complete cds
 l24774_272-757,delta3,_delta2-coa-isomerase mrna, 3' end
 l42583cds_1334-1665:in reversesequence,_305-528,keratinisoform_k6a (krt6a) gene_
 all_m24900_1501-2054,triiodothyronine_receptor (thr1, ear1), and ear2_genes, lastexons_each_
 m27093_2049-2509,nuclear-encoded_mitochondrial_branched_chain_alpha-
10 keto_acid_dehydrogenase_transacy
 m36067mrna_2602-3040,dna_ligase_i mrna, complete cds_
 m73077_2770-3178,glucocorticoid_receptor_repression_factor(grf-1) mrna, complete cds
 m94055_5925-6285,voltage-gated_sodium_channel mrna, complete cds_
 all_u17894_870-1231,alpha(1,2)fucosyltransferase (fut2) gene, complete cds_
15 u38545_3056-3578,arf-activated_phosphatidylcholine-
 specific_phospholipase_d1a (hpld1) mrna, complete
 u45448_2014-2535,p2x1_receptor mrna, complete cds
 u68727_2868-3414,homeobox-containing_protein mrna, complete cds
 u90550_2991-3513,butyrophilin (btf2) mrna, complete cds
20 x76029cds_141-453:in reversesequence,_636-756,mrna_for_neuromedin_u_
 all_x99226_4853-5412,mrna_for_faa_protein

Metagene 158

- 25** m92843_1144-1583,zinc_finger_transcriptional_regulator mrna, complete cds
 u62015_1475-1841,cyr61 mrna, complete cds_
 v01512mrna#2_1533-2061,cellular_oncogene_c-fos (complete_sequence)
 all_x51345_1604-1744,jun-b mrna_for_jun-b_protein
 all_x52541_2549-3102,mrna_for_early_growth_response_protein(hegr1)
30 all_x68277_1459-1952,cl_100 mrna_for_protein_tyrosine_phosphatase
 all_x75918_2858-3417,mrna_for_not

Metagene 146

- 35** x12556mrna_3159-3483,mrna_for_dbl_proto-oncogene_
 all_x52011_699-1144,myf6_gene_encoding_a_muscle_determination_factor_

Metagene 141

u19180_535-925,b_melanoma_antigen_(bage)_mrna,_complete_cds
 u30828_1078-1630,splicing_factor_srp55-2_(srp55)_mrna,_complete_cds
 u51269_3408-3900,armadillo_repeat_protein_mrna,_complete_cds_

5 Metagene 137

af005037_574-
 1030,secretory_carrier_membrane_protein_(scamp1)_mrna,_complete_cds/gb=af005037_/ntype=
 d87449_5359-5785,mrna_for_kiaa0260_gene,_partial_cds_
 10 100972_2064-2202,cystathionine-beta-synthase_(cbs)_mrna
 149218exon_4-
 91,retinoblastoma_susceptibility_protein_(rb1)_e413kbp_deletion_mutant_(resulting_in_pr
 m88163_3059-3581,global_transcription_activator_homologous_sequence_mrna,_complete_cds_
 u79296_1366-1876,dihydrolipoamide_acetyl_transferase_mrna,_partial_cds.

15

Metagene 129

108010exon#6_94-211:not_in_gb_record,reg_gene_homologue,_complete_cds
 l32831exon_463-1036,g_protein-coupled_receptor_(gpr3)_gene,_complete_cds
 20 m19888_58-580,small_proline_rich_protein_(spri)_mrna,_clone_128
 m19989_cds1_at_m19989_m19989,not_in_gb_record,platelet-
 derived_growth_factor_(pdgfa)_a_chain_gene,pl
 all_m59216_1586-2163:in_m59216cds_1091,gamma-aminobutyric_acid-a_(gaba-a)_receptor_beta-
 1_subunit_
 25 u58681cds_807-1116:in_reversesequence,_1191-1434:not_in_gb_record,neurogenic_basic-helix-
 loop-helix_
 all_x63337_548-1101,hb2a_gene_for_high_sulfur_keratin
 z29572cds_52-322:in_reversesequence,_95-605,antisense_mrna_for_bcma_peptide
 z48511exon#4_572-1148,xg_mrna_(clone_pep11)

30

Metagene 88

d13640_4563-5091,mrna_for_kiaa0015_gene,_complete_cds
 hg2414-ht2510_s_at_hg2414-ht2510_prostaglandin_receptor_ep1_subtype
 35 hg3236-ht3413_f_at_hg3236-ht3413_neurofibromatosis_tumor_suppressor
 hg3342-ht3519_s_at_hg3342-ht3519_id1_
 j03801_911-1418,lysozyme_mrna,_complete_cds_with_an_alu_repeat_in_the_3'_flank_
 all_100389_1196-1792,cytochrome_p-450gene_
 m11058mrna_2351-2879,3-hydroxy-3-methylglutaryl_coenzyme_a_reductase_mrna,_complete_cds

- m19045_907-1414,lysozyme_mrna_complete_cds
all_m31551_576-1134,urokinase_inhibitor_(pai-2)_gene_
m31667_f_at_m31667_m31667_4040_in_all_m31667_1679-
2265,cytochrome_p450_(cyp1a2)_gene_
5 u32576mrna_19-535,apolipoprotein_apoc-iv_(apoc4)_gene_complete_cds_
u33267_1613-2081,glycine_receptor_beta_subunit_(glrb)_mrna_complete_cds_
u50361_16-319,calcium_calmodulin-
dependent_protein_kinase_ii_delta_mrna_partial_cds/gb=u50361_/nty
u60269cds#2_171-429,endogenous_retrovirus_herv-
10 k(hml6)_proviral_clone_hml6.17_putative_polymerase_an
u72507mrna_855-1341,40871_mrna_partial_sequence
x14008mrna_926-1433,lysozyme_gene_(ec_3.2.1.17)_
all_x51417_1050-1651,mrna_for_steroid_hormone_receptor_herr2_
y10207mrna_61-475,mrna_for_cd171_protein/gb=y10207_/ntype=rna
15
Metagene 83
d90224_2791-3319,mrna_for_glycoprotein_34_(gp34)_
hg415-ht415_at_hg415-ht415_lectin_galactoside-binding_soluble_2_
20 k03204mrna_582-1130,prb1_locus_salivary_proline-rich_protein_mrna_clone_cp3_complete_cds_
m14758mrna#1_4264-4561,p-glycoprotein_(mdr1)_mrna_complete_cds_
m36653_1448-1663,2-oct_factor_mrna_complete_cds_
m64231mrna_1264-1624,spermidine_synthase_gene_complete_cds_
m64358exon_16-189,rhom-3_gene_exon/gb=m64358_/ntype=dna_/annot=exon_
25 all_u67368_952-1411,multiple_exostosis(ext2)_gene_
all_x16105_1077-1226,mrna_for_rd_protein_rna-binding
x58255mrna_2472-2862,flg-2_gene_for_fibroblast_growth_factor_receptor
all_x67235_1087-1595,mrna_for_proline_rich_homeobox_(prh)_protein
y10209mrna_79-331,mrna_for_cd30l_protein/gb=y10209_/ntype=rna
30 all_z70723_1812-2239,mrna_for_serum_arylidiakylphosphatase
Metagene 65
d29642_2294-2582,mrna_for_kiaa0053_gene_complete_cds
35 hg1155-ht4822_at_hg1155-ht4822_colony-stimulating_factor_1_macrophage_altsplice_3
hg1996-ht2044_at_hg1996-ht2044_guanine_nucleotide-binding_protein_rap2_ras-
oncogene_related_
hg243-ht243_s_at_hg243-ht243_lowe_oculocerebrorenal_syndrome_protein_
hg2797-ht2905_at_hg2797-ht2905_clathrin_light_polypeptide_altsplice_1

- hg4011-ht4804_s_at_hg4011-ht4804_dystrophin-associated_glycoprotein_50_kda_altsplice_2_
hg4757-ht5207_s_at_hg4757-ht5207_oncogene_mll-af4_fusion_activated
j00268gene_270-1415,insulin_gene_
178440mrna_2089-2509,stat4_mrna_complete_cds_
5 m10321mrna_5749-6321,von_willebrand_factor_mrna_3'_end
m34455_1427-1889,interferon-gamma-inducible_indoleamine_2,3-
dioxygenase_(ido)_mrna_complete_cds_
m61827mrna_1289-1850,leukosialin_(cd43)_gene_complete_cds
m74542_1131-1611,aldehyde_dehydrogenase_type_iii_(aldhiii)_mrna_complete_cds
10 all_u24683_219-474,anti-b_cell_autoantibody_igm_heavy_chain_variable_v-d-
j_region_(vh4)_gene_clone_
u34587_1545-2061,corticotropin-releasing_factor_receptormrna_complete_cds
u48861_1914-2430,betanicotinic_acetylcholine_receptor_subunit_mrna_complete_cds
u51096_1240-1720,homeobox_protein_cdx2_mrna_complete_cds
15 all_u58675_25626-39844_or17-
228_gene_extracted_fromolfactory_receptor_gene_cluster_on_chromosome_17
u64315_2269-2832,dna_repair_endonuclease_subunit_(xpf)_mrna_complete_cds
u81600_368-734,paired-like_homeodomain_protein_prx-2_mrna_partial_cds.
u82010mrna_2432-
20 2930_homo_sapiensheme_a_farnesyltransferase_(cox10)_gene_promoter_region_and
x58399mrna_491-903,l2-9_transcript_of_unrearranged_immunoglobulin_v(h)5_pseudogene.
x60003mrna_543-965,delta_creb_mrna_for_camp-responsive_element_(cre)_binding_protein_
all_x63359_2216-2781,ugt2bio_mrna_for_udp_glucuronosyltransferase
x68985cds_482-656,mrna_for_hepatic_leukemia_factor_
25 x72882cds_19-103:in_reversesequence_144-186,14a6ck_dna_sequence
x74764cds_2202-2538:in_reversesequence_2903-3041,mrna_for_receptor_protein_tyrosine_kinase_
x75342cds_1407-1767:in_reversesequence_2095-2239,shb_mrna
all_x84213_1094-1357,bak_mrna_for_bcl-2_homologue
x89416cds_1386-1440:in_reversesequence_1533-1932,mrna_for_protein_phosphatase_5_
30 x91911cds_321-711:in_reversesequence_912-950,mrna_for_rtv-1_protein_
x97267mrna_321-861,lpap_gene
all_x98085_4149-4642,mrna_for_tenascin-r_
all_x99664_723-1276,mrna_for_protein_containing_sh3_domain_sh3gl3_
all_y00796_4559-5109,mrna_for_leukocyte-associated_molecule-1_alpha_subunit_(lfa-
35 1_alpha_subunit)
y08409cds_4-385:in_reversesequence_431,spot14_gene_
y08639cds_837-1353:in_reversesequence_1953-2001,mrna_for_transcription_factor_rzrbeta
y09216_214-736,mrna_for_protein_kinase_dyrk2
all_z11697_1190-1701,mrna_for_hb15

z23115cds_197-677:in_reversesequence_817-835,bcl-xl_mrna_
z67743cds_1792-2320:in_reversesequence_2350,mrna_for_clc-7_chloride_channel_protein

Metagene 57

5

all_141913_305-502,retinoblastoma_susceptibility_protein_(rb1)_gene_exon_26,_bases_174145-
174668_in
all_x75958_1683-2170,trkb_mrna_for_protein-tyrosine_kinase_

10 Metagene 41

hg2441-ht2537_s_at_hg2441-ht2537_retinoblastoma_protein_mutated_
m16282cds_25-133:in_reversesequence_283-
469,fragile_x_locus_m2c_containing_an_unidentified_open_rea
15 all_m17254_1366-1889,erg2_gene_encoding_erg2_protein_complete_cds_
u84540mrna_1083-1341,dystrobrevin_isoform_dtn-
3_(dtn)_gene_exon_11b_and_complete_cds/gb=u84540_/nty
y10202mrna_169-529,mrna_for_cd207_protein/gb=y10202_/ntype=rna_

20 Metagene 37

j04076mrna_2171-2651,early_growth_responseprotein_(egr2)_mrna_complete_cds_
m31659mrna_1130-1640,gt_mitochondrial_solute_carrier_protein_homologue_mrna_complete_cds
all_x95677_1773-2368,mrna_for_argbpib_protein/gb=x95677_/ntype=rna_

25

Metagene 29

d78014_4608-4998,mrna_for_dihydropyrimidinase_related_protein-3_complete_cds
hg2614-ht2710_at_hg2614-ht2710_collagen_type_viii_alpha_1
30 m61906_2813-3326,p13-kinase_associated_p85_mrna_sequence_
u29953mrna_1150-1468,pigment_epithelium-derived_factor_gene_complete_cds_
u40572_1105-1627,beta2-syntrophin_(snt_b2)_mrna_complete_cds
u79294_831-1371,clone_23748_mrna_complete_cds.

x15525mrna_1670-2084,lysosomal_acid_phosphatase_gene_(ec_3.1.3.2)_exon(and_joined_cds)_

35

all_x68742_2942-3423,mrna_for_integrin_alpha_subunit
x96719cds_86-398:in_reversesequence_674-710,mrna_for_aicl_(activation-induced_c-type_lectin)_

Metagene 25

- af001294_285-735,ipl (ipl)_mrna,_complete_cds.
 d16227_589-943,mrna_for_bdp-1_protein_(a_member_of_the_recoverin_family),_complete_cds_
 d50930_4876-5368,mrna_for_kiaa0140_gene,_complete_cds
 d78012_2289-2793,mrna_for_dihydropyrimidinase_related_protein-1,_complete_cds
5 d79985_3997-4393,mrna_for_kiaa0163_gene,_complete_cds
 d90359_5384-5912,ccg1_mrna_
 hg2566-ht4792_r_at_hg2566-ht4792_microtubule-associated_protein_tau,_altsplice_3,_exon_8_
 j03930exon#11_638-1118,intestinal_alkaline_phosphatase_(alpi)_gene,_complete_cds_
 j04469exon#9_11-173:not_in_gb_record,mitochondrial_creatine_kinase_(ckmt)_gene,_complete_cds
10 j05249_941-1409,replication_protein_a_32-kda_subunit_mrna,_complete_cds
 l14856cds_746-1100:in_reversesequence,_1324-1393,somatostatin_receptor_gene,_complete_cds_
 l18983mrna_3114-3588,tyrosine_phosphatase_(ia-2/ptp)_mrna,_complete_cds_
 l27479_797-1307,x123_mrna,_3'_end
 l47345_2141-2609,elongin_a_mrna,_complete_cds_
15 m36430_321-753,transducin_beta-1_subunit_mrna,_3'_end
 m57732mrna_2643-
 3165,hepatic_nuclear_factor(tcfl)_mrna,_complete_cds,_clones_hcl10,_hcl12,_hcl17,_an
 reverse_m81780_4000-4487:in_m81780cds#3_175-
 296,_smpd1_gene_(acid_sphingomyelinase)_extracted_fromac
20 m88468_1378-1906,mevalonate_kinase_mrna,_complete_cds_
 u01147mrna_4659-5211,guanine_nucleotide_regulatory_protein_(abr)_mrna,_complete_cds
 u09584_1382-1835,pl6_protein_(pl6)_mrna,_complete_cds
 u47742_7360-7810,monocytic_leukaemia_zinc_finger_protein_(moz)_mrna,_complete_cds
 u47928_2047-2491,protein_a_alternatively_spliced_form(a-2)_mrna,_complete_cds_
25 u53786_6024-6432:not_in_gb_record,envoplakin_(evpl)_mrna,_complete_cds

Metagene 7

- j00207mrna#2_661-1075,_ifna_gene_(interferon_alpha-
30 a)_extracted_fromleukocyte_interferon_(leif)_alph
 j05016mrna_2252-
 2824,(clone_pa3)_protein_disulfide_isomerase_related_protein_(erp72)_mrna,_complete_
 l41268_f_at_l41268_l41268,_4040_in_l41268mrna_1043-1571,natural_killer-
 associated_transcript(nkat2)_
35 m31776cds_35-365,brain_natriuretic_protein_(bnp)_gene,_complete_cds
 u82311_39-112,unknown_protein_mrna,_partial_cds/gb=u82311_/ntype=rna_
 all_x06661_1817-2340,mrna_for_27-kda_calbindin_
 x13100cds_3130-3466:in_reversesequence,_3496-3592,mrna_fragment_for_myosin_heavy_chain
 x64994cds_642-912:in_reversesequence,_1279-1471,hgmp07i_gene_for_olfactory_receptor_

Metagene 6

- hg1139-ht4910_at_hg1139-ht4910_fk506-binding_protein,_altsplice_2
 5 m14123cds#4_3521-3935,_pol_fromendogenous_retrovirus_herv-
 k10/gb=m14123_/ntype=dna_/annot=cds,_pol_f
 m27396mrna_1389-1842,asparagine_synthetase_mrna,_complete_cds
 m89470_2855-3271,paired-box_protein_(pax2)_mrna,_complete_cds
 s73885_1537-2082,_ap-4=basic_helix-loop-helix_dna-
 10 binding_protein_[human,_cervical_carcinoma,_hela_c
 u35005_764-1278,jnk1_beta2_protein_kinase_(jnk1b2)_mrna,_complete_cds
 u51333_2437-3005,hexokinase_iii_(hk3)_mrna,_complete_cds_
 u73738_74-107,calcium/calmodulin-
 dependent_protein_kinase_ii_delta_e_mrna,_partial_cds/gb=u73738_/nt

15

Metagene 44

- hg3733-ht4003_at_hg3733-ht4003_epiligrin,_alpha_3
 m65291_715-1189,natural_killer_cell_stimulatory_factor_(nksf)_mrna,_complete_cds,_clone_p35
 20 u15422cds#2_17-269:in_reversesequence,_20347-
 20563,_prm2_gene_(protamine_2)_extracted_fromprotamine(
 u18297_1298-1805,mst1_(mst1)_mrna,_complete_cds

Metagene 461

25

- hg4340-ht4610_at_hg4340-ht4610_soxa
 u63332_3-361,super_cysteine_rich_protein_mrna,_partial_cds.
 u77413_2543-2975,o-linked_glcnae_transferase_mrna,_complete_cds/gb=u77413_/ntype=rna_
 x97675mrna_3636-4212,_plakophilin_2a_gene_extracted_frommrna_for_plakophilin_2a_and_b_
 30 all_z80781_583-748,h2b/j_gene

Metagene 418

- hg458-ht458_f_at_hg458-ht458_beta-1-glycoprotein_1,_pregnancy-specific_
 35 m22324_2954-3416,aminopeptidase_n/cd13_mrna_encoding_aminopeptidase_n,_complete_cds
 u04343_815-1361,cd86_antigen_mrna,_complete_cds
 u20760_4534-4966,extracellular_calcium-sensing_receptor_mrna,_complete_cds_
 u67849_25-187,beta-galactoside_alpha2,6-
 sialyltransferase_(sialt1)_mrna,_exon_w/gb=u67849_/ntype=rna

x59372mrna_610-1090,hox4c_mrna_for_a_homeobox_protein
 x65614cds_10-262:in_reversesequence,_19-391,mrna_for_calcium-binding_protein_s100p_
 x81892cds_2760-2994:in_reversesequence,_3126-3204,mrna_for_he6_tm7_receptor_
 all_x95525_2560-3071,mrna_for_tafii100_protein_

5

Metagene 413

all_u03877_2037-2512,extracellular_protein_(s1-5)_mrna,_complete_cds_

10 Metagene 329

m27968mrna_3289-3658,basic_fibroblast_growth_factor_(fgf)_mrna,_complete_cds_
 all_m31994_117-538,cytosolic_aldehyde_dehydrogenase_(aldh1)_gene_
 m73780_3266-3746,integrin_beta-8_subunit_mrna,_complete_cds
 u20860exon#3_1889-2279,angiotensin_ii_typereceptor_gene,_complete_cds_
 u65002_6724-7240,zinc_finger_protein_plagl1_mrna,_complete_cds
 all_x04688_227-798,mrna_for_t-cell_replacing_factor_(interleukin-5)

Metagene 317

20

j03242_1155-1324,insulin-like_growth_factor_ii_mrna,_complete_cds_
 j05068_984-1494,transcobalamin_i_mrna,_complete_cds
 m32578_1131-1191,mhc_ii_hla-dr_beta-1_mrna_(dr2.3),_5'_end_
 all_x79981_3411-3946,ve-cadherin_mrna

25

Metagene 271

m10901mrna_4325-4655,glucocorticoid_receptor_alpha_mrna,_complete_cds
 m88338_1465-1867,serum_constituent_protein_(mse55)_mrna,_complete_cds ,
 u03891_90-576,phorbolin_i_mrna,_partial_cds
 u77643_1462-1972,k12_protein_precursor_mrna,_complete_cds
 x74795cds_1923-2181:in_reversesequence,_2272-2488,p1-cdc46_mrna_
 all_x78669_1114-1643,erc-55_mrna_

35 Metagene 245

y09912mrna_757-1315,ap-2_beta_gene

Metagene 185

af009301_2752-3262,teb4_protein_mrna,_complete_cds/gb=af009301_/ntype=rna_
u73304mrna_4973-5447,cbl_cannabinoid_receptor_(cnr1)_gene,_complete_cds.
x53414mrna_907-1453,mrna_for_peroxisomal_l-alanine:glyoxylate_aminotransferase_
5 x59739mrna_5061-5473,zfx_mrna_for_puttranscription_activator,_isoform_2
x60955cds_2-147:in_reversesequence,_154-168,tyrrp_gene_for_tyrosinase-related_protein_(trp-
1)_(parti

Metagene 163

10

d63882_1015-1568,hslim15_mrna_for_hslim15,_complete_cds
hg2188-ht2258_at_hg2188-ht2258_paired_box_hup1_
m37825_624-1044,fibroblast_growth_factor-5_(fgf-5)_mrna,_complete_cds
m60092mrna_1743-2295,myoadenylate_deaminase_(ampd1)_mrna,_complete_cds_
15 s67798_1420-1930,_ph-20_[human,_testis,_mrna,_1973_nt]
u49065_1400-1922,interleukin-1_receptor-
related_protein_mrna,_complete_cds/gb=u49065_/ntype=rna
u82671mrna#2_1536-1776:in_reversesequence,_106561-106657,_hsp1-
a_gene_extracted_fromcosmids_qc14e2,_
20 all_u83303_1160-2035,_gcp-2_gene_(granulocyte_chemotactic_protein-2)_extracted_fromline-
1_reverse_tr
all_x91148_3331-3824,mrna_for_microsomal_triglyceride_transfer_protein_

Metagene 103

25

u59877_295-750,low-mr_gtp-binding_protein_(rab31)_mrna,_complete_cds_
x51441cds_28-
65:in_reversesequence,_228,mrna_for_serum_amyloid_a_(saa)_protein_partial,_clone_pas3-a
all_x52075_5011-5273,gene_for_sialophorin_(cd43)
30 all_z11559_2897-3480,mrna_for_iron_regulatory_factor_
all_z29331_1560-1981,(23k/3)_mrna_for_ubiquitin-conjugating_enzyme_ubch2_

Metagene 80

35

hg2479-ht2575_at_hg2479-ht2575_helix-loop-helix_protein_sef2-1d
m55682cds_1132-1467:in_reversesequence,_439-571,carilage_matrix_protein_(cmp)_gene_
s77583_4-
66,_hervk10/hummtv_reverse_transcriptase_homolog_{clone_rt244}_{human,_multiple_sclerosis,_

Metagene 55

d13626_1857-2373,mrna_for_kiaa0001_gene,_complete_cds

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Metagene 417

hg3299-ht3476_at_hg3299-ht3476_acetyl-coenzyme_a_carboxylase_
u79265_1269-1623,clone_23614_mrna_sequence_

10 x12901cds_2080-2431:in_reversesequence,_2551-2629,mrna_for_villin_

Metagene 287

15 d17525mrna_3966-4446,mrna_for_precursor_of_p100_serine_protease_of_ra-
reactive_factor,_complete_cds

d28483_944-1466,scr3_mrna_for_rna_binding_protein_scr3,_complete_cds_

d28532_1223-1763,mrna_for_renal_na⁺-dependent_phosphate_cotransporter,_complete_cds

d31628cds_781-1132,gene_for_4-hydroxyphenylpyruvic_acid_dioxygenase(hpd),_complete_cds_

hg2707-ht2803_at_hg2707-ht2803_serine/threonine_kinase_

20 j04990cds_371-683:in_reversesequence,_2929-2989,cathepsin_g_gene,_complete_cds

j05257_1239-1713,(clones_mdp4,_mdp7)_microsomal_dipeptidase(mdp)_mrna,_complete_cds

l02321_1089-1509,glutathione_s-transferase(gstm5)_mrna,_complete_cds

l08485_1759-2257,gaba-benzodiazepine_receptor_alpha-5-subunit(gabra5)_mrna,_complete_cds

m34065mrna_1526-1952,cdc25hs_mrna,_complete_cds

25 s68287_662-1124,_chlordecone_reductase_{clone_hakra}_{human,_liver,_mrna,_1167_nt]

u64863_1556-2030,hpd-1_(hpd-1)_mrna,_complete_cds

Metagene 225

30 d21205_1715-2279,mrna_for_estrogen_responsive_finger_protein,_complete_cds_

hg2271-ht2367_s_at_hg2271-ht2367_profilaggrin

hg2981-ht3125_s_at_hg2981-ht3125_epican,_altsplice_1_

l17330_88-586,pre-t/nk_cell_associated_protein_(6h9a)_mrna,_complete_cds_

l76927mrna_760-1330,galactokinase(galk1)_gene,_complete_cds

35 m31520mrna_2-

l31,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna_

u52111mrna#3_2176-

2659,xq28_genomic_dna_in_the_region_of_the_ald_locus_containing_the_genes_for_crea

u57317_2551-2989,p300/cbp-associated_factor_(p/caf)_mrna,_complete_cds_

u66468_586-1126,cell_growth_regulator_cgr11_mrna,_complete_cds_

Metagene 169

- 5** d50928_2629-3019,mrna_for_kiaa0138_gene,_complete_cds
hg2417-ht2513_at_hg2417-ht2513_dynein,_heavy_chain,_cytoplasmic
m15958cds_12-282:in_reversesequence,_6718-6778,gastrin_gene,_complete_cds_
u68162mrna_3059-
3585,_mpl_gene_(thrombopoietin_receptor)_extracted_fromthrombopoietin_receptor_(mpl)
- 10** all_x60484_683-858,h4/e_gene_for_h4_histone
x68505_2403-2879,mrna_for_myocyte-specific_enhancer_factor(mef2)

Metagene 132

- 15** d37781_4150-4705,mrna_for_protein-tyrosine_phosphatase_hptpeta,_complete_cds_
j00209mrna_366-878,leukocyte_interferon_(ifn-alpha)_alpha-c_mrna,complete_cds
m90696_1168-1738,cathepsin_s_(ctss)_mrna,_complete_cds_
u03735exon#3_970-1517,mage-3_antigen_(mage-3)_gene,_complete_cds_

20 Metagene 105

u38276_2969-3509,semaphorin_iii_family_homolog_mrna,_complete_cds
all_x17093_3834-4023,hla-f_gene_forleukocyte_antigen_f
all_x59798_3705-4192,prad1_mrna_for_cyclin_

25

Metagene 104

- d78611_1893-2331,mest_mrna,_complete_cds_
l01406_1010-1562,growth_hormone-releasing_hormone_receptor_mrna,_complete_cds
30 m20919cds_478-568:in_reversesequence,_899-
927,dna_with_a_hepatitis_b_virus_surface_antigen_(hbsag)_g

Metagene 24

- 35** l34357_1655-2165,gata-4_mrna,_complete_cds
u09860_3095-3653,enterokinase_mrna,_complete_cds_
u33448cds_773-1108:in_reversesequence,_1666-1883,putative_g-protein-
coupled_receptor_(gpr16)_gene,_c
u40370_1443-1929,3',5'_cyclic_nucleotide_phosphodiesterase_(hspde1a3a)_mrna,_complete_cds_

all_x02750_1332-1729,liver_mrna_for_protein_c
 z47727cds_6-150;in_reversesequence,_28-313,mrna_for_rna_polymerase_ii_subunit
 z80780cds_2-339,h2b/h_gene.

5 Metagene 366

- ad000092cds#7_730-1062;in_reversesequence,_99587-99822,_hypotheticalserine-
 threonine_protein_kinase_
 d50405_1628-2054,mrna_for_rpd3_protein,_complete_cds_
 10 d50925_3408-3918,mrna_for_kiaa0135_gene,_partial_cds_
 d87442_2204-2684,mrna_for_kiaa0253_gene,_partial_cds_
 104490_954-1362,(clone_cc6)_nadh-ubiquinone_oxidoreductase_subunit_mrna,_3'_end_cds_
 l37033_1039-1480,fk-506_binding_protein_homologue_(fkbp38)_mrna,_complete_cds
 m92269cds_6175-6626;in_reversesequence,_6958-7053,l-
 15 type_calcium_channel_hfcc_mrna,_complete_cds
 u94585_1810-2308,requiem_homolog_(hsreq)_mrna,_complete_cds.
 all_x02596_4186-
 4733,mrna_for_bcr_(breakpoint_cluster_region)_gene_in_philadelphia_chromosome
 all_x69550_1266-1801,mrna_for_rho_gdp-dissociation_inhibitor_1_
 20 x80200_1428-1866,mln62_mrna
 all_x80497_3995-4428,phkla_mrna
 z21488cds_2749-3016;in_reversesequence,_3179-3326,contactin_mrna
 all_z48054_2544-3067,mrna_for_peroxisomal_targeting_signal(skl_type)_receptor_

25 Metagene 121

- d00749exon_346-525,t_cell_surface_antigen_cd7_gene_
 hg1877-ht1917_s_at_hg1877-ht1917_myelin_basic_protein,_altsplice_form_4
 hg4126-ht4396_at_hg4126-ht4396_zinc_finger_protein_hzf4
 30 m97287_2345-2885,mar/sar_dna_binding_protein_(satb1)_mrna,_complete_cds
 x98178cds_567-607,mrna_for_mach-beta-4_protein/gb=x98178_/ntype=rna
 y07755exon#2-3_16-204,s100a2_gene,_exon_1,and_3_
 z30426_at_z30426_z30426,not_in_gb_record,gene_for_early_lymphocyte_activation_antigen_cd69,
 _exon_1

35

Metagene 49

hg4316-ht4586_at_hg4316-ht4586_transketolase-like_protein

Metagene 382

- hg4458-ht4727_at_hg4458-ht4727_immunoglobulin_heavy_chain_vdjc_regions
 all_l00058_470-855,(gh)_germline_c-myc_proto-oncogene_5'_flank
5 u16258_1212-1776,i_kappa_br_mrna,_complete_cds_
 all_x82629_1744-2297,mrna_for_mox-2
 x97324cds_749-1277,mrna_for_adipophilin/gb=x97324_/ntype=rna_

Metagene 365

- 10**
 ad001527cds#1_317-575:in_reversesequence,_3640-3802,_comment_for_location_3447-3655:_blastx_gil10329
 m31423cds_322-640:in_reversesequence,_1200-1320,cerebellar-degeneration-related_antigen_(cdr34)_gene
15 u44060_2395-2845,homeodomain_protein_(prox_1)_mrna,_complete_cds_
 u57093_501-969,small_gtp-binding_protein_rab27b_mrna,_complete_cds_

Metagene 281

- 20** d28235exon#10_1923-2282,ptgs2_gene_for_prostaglandin_endoperoxide_synthase-2,_complete_cds_
 all_k02545_752-1044,_tcrb_gene_extracted_fromt-cell_receptor_germline_beta-chain_j-beta-1_gene_clust
 all_x98330_15142-15731,mrna_for_ryanodine_receptor_2_

25

Metagene 180

- m21188mrna_2754-3204,insulin-degrading_enzyme_(ide)_mrna,_complete_cds_
 s66896_1272-
30 1638,_squamous_cell_carcinoma_antigen=serine_protease_inhibitor_[human,_mrna,_1711_nt]
 u06452_923-1475,melanoma_antigen_recognized_by_t-cells_(mart-1)_mrna_
 u13616_14235-14709,ankyrin_g_(ank-3)_mrna,_complete_cds
 all_x70340_3545-4062,mrna_for_transforming_growth_factor_alpha_

35 Metagene 155

- m26683_416-510,interferon_gamma_treatment_inducible_mrna_
 m60314_1582-2044,transforming_growth_factor-beta_(tgf-beta)_mrna,_complete_cds_
 u02310_2946-3372,fork_head_domain_protein_(fkhf)_mrna,_complete_cds

u57796_3322-3784,zinc_finger_protein_(ld5-1)_mrna,_complete_cds
all_u60116_905-966:not_in_gb_record,skeletal_muscle_lim-protein_slim2_mrna,_partial_cds_

Metagene 79

5

u00802_1922-2463,drebrin_e2_mrna_(dbn1),_complete_cds
u77594_245-599,tazarotene-induced_gene(tig2)_mrna,_complete_cds_
u86136_8094-8472,telomerase-associated_protein_tp-1_mrna,_complete_cds_
x82494mrna_3527-3965,mrna_for_fibulin-2

10

Metagene 186

m11726exon#1_49-163;in_reversesequence,_1559-

15

2534:not_in_gb_record,pancreatic_polypeptide_gene,_comp
u15590_306-840,heat_shock_protein_27_(hsp27)_mrna,_complete_cds

Metagene 166

20

af001359_2-
27,dna_mismatch_repair_protein_(hmlh1)_mrna,_alternatively_spliced,_partial_cds/gb=af0013
hg627-ht5097_s_at_hg627-ht5097_rhesus_(rh)_blood_group_system_ce-antigen,_altsplice_2,_rhvi
hg627-ht5098_s_at_hg627-ht5098_rhesus_(rh)_blood_group_system_ce-
antigenl,_altsplice_3,_rhviii_

25

105144_2488-2598,(clone_lamda-hpec-
3)_phosphoenolpyruvate_carboxykinase_(pck1)_mrna,_complete_cds_
all_105187_2284-2339,small_proline-rich_protein(sprrla)_gene,_complete_cds_
118877exon#2_980-1530,mage-12_protein_gene,_complete_cds_
120469_499-996,truncated_dopamine_d3_receptor_mrna,_complete_cds.

30

m23323mrna_779-1309,membrane_protein_(cd3-epsilon)_gene
s72503_1692-
1870,_hrk1=inward_rectifier_potassium_channel_[human,_hippocampus,_mrna,_1913_nt]
u12707_1280-1744,wiskott-aldrich_syndrome_protein_(wasp)_mrna,_complete_cds
u15641_760-1283,transcription_factor_e2f-4_mrna,_complete_cds

35

u20979_2612-3068,chromatin_assembly_factor-i_p150_subunit_mrna,_complete_cds_
u73167cds#2_79-
834,_h_luca14.2a_gene_extracted_fromcosmid_luca14,_h_luca14.2a_gene_extracted_fromcos
x87344mrna#26_769-945,dma,_dmb,_hla-
z1,_ipp2,_lmp2,_tap1,_lmp7,_tap2,_dob,_dqb2_and_ring8,_9,andgene

x97064cds_1988-2210:in_reversesequence,_2435-2678,mrna_for_sec23a_isoform,_2748bp
 z30644cds_1860-1918:in_reversesequence,_2130-
 2138,mrna_for_chloride_channel_(putative)_2163bp_

5 Metagene 34

hg3992-ht4262_at_hg3992-ht4262_cpg-enriched_dna_clone_e35_
 j02843cds_1103-1451:in_reversesequence,_14089-14119,cytochrome_p450iie1_(ethanol-
 inducible)_gene_co

- 10 m54927mrna_2349-2907,myelin_proteolipid_protein_mrna_complete_cds_
 u38480_1008-1521,retinoid_x_receptor-gamma_mrna_complete_cds
 x05608exon#4_172-406:not_in_gb_record,gene_for_neurofilament_subunit_nf-l_

Metagene 22

15

af001787_990-1150,uncoupling_proteinmrna_complete_cds/gb=af001787/_ntype=rna
 s81957mrna#1_40-112,_bmp-5=bone_morphogenic_protein-
 5_{promoter}_[human_genomic,_1116_nt]/gb=s81957
 all_x55777_1833-

- 20 2326,_putorf_gene_extracted_frommahlavu_hepatocellular_carcinoma_hhc(m)_dna_

Metagene 323

l49229cds_2-

- 25 87,retinoblastoma_susceptibility_protein_(rb1)_gene,_with_abp_deletion_in_exon_22_(11191
 y09305cds_267-675:in_reversesequence,_711-771,mrna_for_protein_kinase,_dyrk4,_partial_
 y10517mrna_252-606,mrna_for_cd108_protein/gb=y10517/_ntype=rna_

Metagene 266

30

u18467_1436-1946,pregnancy-specific_beta_1-glycoprotein(psg7)_mrna_complete_cds
 u65918_1248-1820,putative_rna_binding_protein_(dazh)_mrna_complete_cds
 z78290_44-109,mrna_(clone_1d7).

35 Metagene 94

u66581cds_963-1275:in_reversesequence,_1547-1745,putative_g_protein-
 coupled_receptor_(gpr22)_gene_c
 u73799_34-265,dynactin_mrna_partial_cds/gb=u73799/_ntype=rna

- u88892_31-241,tenascin-c_mrna,_splice_variant_tncfn-ad2,_partial_cds/gb=u88892/_ntype=rna
 all_x73501_11784-13955,gene_for_cytokeratin_20_
 x97249cds_1720-2230,mrna_for_leucine-rich_primary_response_protein_1_
 all_x97261_25-333,mrna_for_metallothionein_isoform_1r,mrna_for_metallothionein_isoform_1r_
5 all_z32684_4621-5042,xk_mrna_for_membrane_transport_protein

Metagene 285

- d37931_395-911,mrna_for_mase_4,_complete_cds
10 hg3731-ht4001_at_hg3731-ht4001_immunoglobulin_heavy_chain_vdjrc_regions_
 hg4668-ht5083_s_at_hg4668-ht5083_transcription_factor_mef2,_altsplice_2
 l23333_725-1305,corticotropin_releasing_factor_receptor_mrna,_complete_cds.
 l38503_531-993,glutathione_s-transferase_theta(gstt2)_mrna,_complete_cds_
 m13981_1253-1300,inhibin_a-subunit_mrna,_complete_cds
15 all_m35093_2155-2456,secreted_epithelial_tumor_mucin_antigen_(muc1)_gene,_complete_cds_
 u15932_1928-2294,dual-specificity_protein_phosphatase_mrna,_complete_cds_
 u79249_873-1359,clone_23839_mrna_sequence
 x65727cds#1_199-591,_gstalpha_locus_gene_(glutathione_s-
 transferase)_extracted_fromgstalpha_gene_for
20 all_x77166_798-1183,gene_for_kunitz-type_protease_inhibitor,_hkib9_
 x95097mrna_924-1503,mrna_for_vip2_receptor
 all_z46261_490-899,dna_for_histone_h3a_

Metagene 367

- 25**
 hg4236-ht4506_f_at_hg4236-ht4506_zinc_finger_protein_znf138
 l32606_1862-2196,homeobox-like_mrna
 m61826exon_72-568,alpha-spectrin_gene
 u09279_1375-1777,type_xix_collagen_(coll9a1)_mrna,_partial_cds_
30 u38964cds_1096-1146:in_reversesequence,_1291-
 1359,pms2_related_(hpmsr2)_gene,_complete_cds_
 u79301_999-1509,clone_23842_mrna_sequence
 x00540_at_x00540_x00540,not_in_gb_record,gene_encoding_prolactin,_exonand_joined_cds_
 all_x15088_1146-1276,gnat1_mrna_for_transducin_alpha-chain_
35

Metagene 269

- hg3985-ht4255_at_hg3985-ht4255_cpg-enriched_dna,_clone_e04_
 m16967_6338-6806,coagulation_factor_v_mrna,_complete_cds_

m59941_2557-2965,gm-csf_receptor_beta_chain_mrna,_complete_cds_
u00672_3067-3577,interleukin-10_receptor_mrna,_complete_cds
u79526_1787-2327,orphan_g-protein_coupled_receptor_dez_isoform_a_mrna,_complete_cds
reverse_z49208_20545-

5 20696,dna_from_cosmid_1161a8,_huntington_disease_region,_chromosome_4p16.3

Metagene 30

- j04132_919-1417,t_cell_receptor_zeta-chain_mrna,_complete_cds
10 m76559_3065-3521,neuronal_dhp-sensitive,_voltage-dependent,_calcium_channel_alpha-
2b_subunit_mrna,_c
m81882mrna_1835-2261,glutamate_decarboxylase_(gad65)_mrna,_complete_cds
s68874_113-469,_ep3_prostanoid_receptor_ep3-
i_{3'_region,_alternatively_spliced}_[human,_mrna_partia
15 u00921exon#3_273-313:not_in_gb_record,lst-1_gene,_complete_cds_
u01828_5837-5942,microtubule-associated_protein(map2)_mrna,_complete_cds
u20759_3683-3758,parathyroid_cell_calcium-sensing_receptor_mrna,_complete_cds
u29943_1609-2065,elav-like_neuronal_protein-2_hel-n2_mrna,_complete_cds
u31628_1015-1507,interleukin-15_receptor_alpha_chain_precursor_(il15ra)_mrna,_complete_cds_
20 x02883exon#4_568-736,gene_for_t-
cell_receptor_alpha_chain_c_region/gb=x02883_/ntype=dna_/annot=exon
all_x70811_2067-2566,mrna_for_betaadrenergic_receptor_
all_x81832_1592-2163,mrna_for_glucose-dependant_insulinotropic_polypeptide_receptor_gene_
x86570_1208-1532,mrna_for_acidic_hair_keratin_1
25 y07683_951-1413,mrna_for_p2x3_purinoreceptor/gb=y07683_/ntype=rna

Metagene 115

- all_m16441_2260-
30 2855,_lymphotoxin_gene_extracted_fromtumor_necrosis_factor_and_lymphotoxin_genes,_co

Metagene 23

- all_x77748_2815-3296,mrna_for_metabotropic_glutamate_receptor_type_3_
35 x84003cds_140-305:in_reversesequence,_373-379,tafi18_mrna_for_transcription_factor_tfiid_
y10510mrna_13-268,mrna_for_cd67s_protein/gb=y10510_/ntype=rna

Metagene 405

- ab000381exon#2-4_45-395: not_in_gb_record,dna_for_gpi-anchored_molecule-like_protein,_complete_cds_
all_d16154_2725-2751: not_in_gb_record,gene_for_cytochrome_p-450c11,_exon_3-9/gb=d16154_/ntype=dna_/a
- 5** j02982_23-439,glycophorin_b_mrna,_complete_cds_
l10373_1311-1713,(clone_ccg-b7)_mrna_sequence
l21893_1039-1537,na/taurocholate_cotransporting_polypeptide_mrna,_complete_cds_
m13928mrna_542-1020,delta-aminolevulinate_dehydratase_mrna,_complete_cds.
all_m29037_3259-3548,_humanbeta-hydroxysteroid_dehydrogenase_(17bhsdi)_gene,_exons_1-5,_complete_cds
s78825_523-667,_id1_(id1-b)=transcription_regulator_helix-loop-helix_protein_{alternatively_spliced}
u12424_2016-2564,mitochondrial_glycerol-3-phosphate_dehydrogenase_mrna,_complete_cds_
u61276_4243-4777,transmembrane_protein_jagged(hj1)_mrna,_complete_cds_
- 10** all_u83598_780-815,death_domain_receptorsoluble_form_(ddr3)_mrna,_partial_cds,death_domain_receptors
v01510mrna_506-1022,_pomc_gene_(proopiomelanocortin)_extracted_fromgene_coding_for_acth_and_beta-lph
x92493mrna_2160-2672,mrna_for_stm-7_protein
- 15** y10511mrna_16-343,mrna_for_cd176_protein/gb=y10511_/ntype=ma
- 20** Metagene 4
- ac002477cds_444-988,pac_clone_dj327a19_from_xq25-q26,_complete_sequence/gb=ac002477_/ntype=dna_/anno
hg4243-ht4513_at_hg4243-ht4513_zinc_finger_protein_znf155
j00129mrna#1_1282-1552: not_in_gb_record,fibrinogen_beta-chain_mrna,_partial_cds_
all_m58026_831-1240,nb-1_mrna,_complete_cds
u30255_977-1493,phosphogluconate_dehydrogenase_(hpgdh)_gene,_complete_cds
- 25** u37022mrna_860-1322,cyclin-dependent_kinase(cdk4)_gene,_complete_cds_
u67191_3391-3967,multiple_exostosis-like_protein_(extl)_mrna,_complete_cds_
u67369_2300-2720,growth_factor_independence-1_(gfi-1)_mrna,_complete_cds_
u85245_3310-3718,phosphatidylinositol-4-phosphate_5-kinase_type_ii_beta_mrna,_complete_cds.
u97018_3439-3853,echinoderm_microtubule-associated_protein_homolog_huemap_mrna,_complete_cds
- 30** x13461cds_88-422:in_reversesequence,_1502-1737,intronless_calmodulin-like_gene_(clp_gene)_for_calmod
all_x72632_1746-2326,mrna_encoding_rev-erbaalpha_(internal_fragment).
z48314cds_2683-3086:in_reversesequence,_3110-3249,mrna_for_apomucin_
- 35**

Metagene 410

- d17547_2106-2262,mrna_for_dopachrome_tautomerase_(tyrosinase-related_protein-
 5 2),_complete_cds
 k02054mrna_238-676,gastrin-releasing_peptide_mrna,_complete_cds
 l33404_464-890,stratum_corneum_chymotryptic_enzyme_mrna,_complete_cds
 m64108_2031-2571,udulinmrna,_3'_end_
 s83198_412-916,_bplp=basic_proline-rich_protein_[human,_lacrimal_gland,_mrna,_947_nt]_
 10 u60206_1537-2003,stress_responsive_serine/threonine_protein_kinase_krs-1_mrna,_complete_cds
 u73960_566-1022,adp-ribosylation_factor-like_proteinmrna,_complete_cds

Metagene 398

- hg2507-ht2603_at_hg2507-ht2603_potassium_channel,_voltage-gated_kcnc1
 j03258mrna_4003-4561,vitamin_d_receptor_mrna,_complete_cds_
 k02268mrna_3155-3677,enkephalin_b_(enkb)_gene,_5'_flank_and
 l05606_1219-1741,myosin_binding_protein_h_mrna,_complete_cds_
 l12392_9795-10257,huntington_disease_(hd)_mrna,_complete_cds
 20 l15533mrna_236-764,pancreatitis-associated_protein_(pap)_gene,_complete_cds_
 l76380mrna_2459-2969,(clone_hsnme29)_cgrp_typerereceptor_mrna,_complete_cds
 all_m16424_135-664,beta-hexosaminidase_alpha_chain_(hexa)_gene_
 s78296_2596-3076,_neurofilament-66_[human,_fetal_brain,_mrna,_3197_nt]
 u57092_317-779,small_gtp-binding_protein_rab30_
 25 u76369_13-325,cationic_amino_acid_transporter-
 2b_(atrc2)_mrna,_partial_cds/gb=u76369/_ntype=rna
 x52425mrna_3032-3536,il-4-r_mrna_for_the_interleukinreceptor

Metagene 309

- 30 d88146_1156-1408,mrna_for_udp-galactose_transporter_2,_complete_cds
 hg2175-ht2245_s_at_hg2175-ht2245_myosin_heavy_polypeptide_10,_non-muscle
 hg3991-ht4261_at_hg3991-ht4261_cpg-enriched_dna_clone_e18_
 all_m19989_804-1279,platelet-derived_growth_factor_(pdgfa)_a_chain_gene,platelet-
 35 derived_growth_fact
 u30313_372-756,diadenosine_tetraphosphatase_mrna,_complete_cds/gb=u30313/_ntype=rna
 u66077_1401-1822,daz_mrna,_3'_utr
 u79272_699-1179,clone_23720_mrna_sequence

x98337cds_643-971:in_reversesequence,_1061-1256,mrna_for_complement_factor_h-related_protein_4

Metagene 214

5

d26135_3247-3619,mrna_for_diacylglycerol_kinase_gamma_complete_cds
hg3105-ht3281_s_at_hg3105-ht3281_atpase_cu2+_transporting_
s78774_411-717,_na+/ca2+_exchanger_[human,_neuroblastoma_x_glioma_hybrid_ng108-15_cells,_mrna_partia

10 x98225cds_31-331,mrna_for_gastrin-binding_protein/gb=x98225_/ntype=rna_

Metagene 38

d21267mrna_1481-1979,mrna_for_highly_expressed_protein_
15 d83781_4231-4729,mrna_for_kiaa0197_gene_partial_cds_
hg3930-ht4200_at_hg3930-ht4200_stearoyl-coenzyme_a_desaturase_
142176_844-1384,(clone_35.3)_dral_mrna_complete_cds
149054_587-1067,t(3;5)(q25.1;p34)_fusion_gene_npm-mifl_mrna_complete_cds.
m95167mrna_3333-3897,dopamine_transporter_(slc6a3)_mrna_complete_cds_
20 u32376_2548-3028,channel_associated_protein_of_synapse_(chapsyn-110)_mrna_complete_cds
x78712cds_1319-1637:in_reversesequence,_1691-1823,mrna_for_glycerol_kinase_testis_specific_2
x82209_7019-7511,mn1_mrna
y10505mrna_94-658,mrna_for_cd104_protein/gb=y10505_/ntype=rna

25 Metagene 456

u30246_3599-4019,bumetanide-sensitive_na-k-cl_cotransporter_(nkcc1)_mrna_complete_cds_

Metagene 153

30

hg4245-ht4515_at_hg4245-ht4515_forkhead_family_afx1
m84349mrna_1366-1852,transmembrane_protein_(cd59)_gene_

Metagene 422

35

d14678_1244-1748,mrna_for_kinesin-related_protein_partial_cds_
d31833_1212-1768,mrna_for_vasopressin_v1b_receptor_complete_cds_
d86043_1741-1829,mrna_for_shps-1_complete_cds_
103427_4325-4844,zinc_finger_protein_basonuclin_mrna_complete_cds_

- 115344_1360-1768,high_molecular_weight_b_cell_growth_factor_mrna_sequence
 m85165_1311-1809,srf_accessory_protein_1a_(sap-1)_mrna,_complete_cds
 m95936_1148-1466,protein-serine/threonine_(akt2)_mrna,_complete_cds
 s78271_4580-5111,_sb1.8/dxs423e=mitosis-
- 5 specific_chromosome_segregation_protein_smc1_homolog_[human,
 u03905_1438-1858,monocyte_chemoattractant_proteinreceptor_(mcp-
 1rb)_alternatively_spliced_mrna,_comp
 u09002_5527-6082,n-methyl-d-
 aspartate_receptor_modulatory_subunit_2a_(hnr2a)_mrna,_complete_cds
- 10 u13395_994-1450,oxidoreductase_(hhcma56)_mrna,_complete_cds
 u28281_1162-1618,secretin_receptor_mrna,_complete_cds
 u50531_4295-4847,brca2_region,_mrna_sequence_cg030_
 u66618_1518-2016,swi/snf_complex_60_kda_subunit_(baf60b)_mrna,_complete_cds
 u85767_13-505,myeloid_progenitor_inhibitory_factor-1_mpif-1_mrna,_complete_cds_
- 15 x14767mrna_1685-1832,mrna_for_gaba-a_receptor,_betasubunit

Metagene 272

- m86917_2402-2972,oxysterol-binding_protein_(osbp)_mrna,_complete_cds_
 20 u19142_69-510,gage-1_protein_mrna,_complete_cds
 u30872_9600-10116,mitosin_mrna,_complete_cds_
 all_u66061_134531-176445,germline_t-
 cell_receptor_beta_chain_tcrbv17slalt,_tcrbv2s1,_tcrbv10slp,_tcr
 u79297_1095-1575,clone_23589_mrna_sequence_
 25 u90268_1427-1703,krit1_mrna,_complete_cds
 all_x07024_4938-5257,x_chromosome_mrna_for_ccg1_protein_invin_cell_proliferation
 x16504cds_781-1266:in_reversesequence,_1283-1354,eno3_mrna_for_beta-enolase_(ec_4.2.1.11).

Metagene 258

- 30 ab000816_783-1357,mrna_for_bmal1d,_partial_cds/gb=ab000816_/ntype=rna
 d17716_1820-2390,mrna_for_n-
 acetylglucosaminyltransferase_v,_complete_cds/gb=d17716_/ntype=rna_
 d25539_3997-4375,mrna_for_kiaa0040_gene,_complete_cds
- 35 hg742-hf742_at_hg742-hf742_latent_membrane_protein_lmp1
 l07597_2496-3036,ribosomal_protein_s6_kinase(rps6ka2)_mrna,_complete_cds_
 m10014cds#1_1048-1264:in_reversesequence,_9512-9722,fibrinogen_gamma_chain_and_gamma-
 prime_chain_gen
 m28825_1513-2047,thymocyte_antigen_cd1a_mrna,_complete_cds_

- u03274_1497-1941,biotinidase_mrna,_complete_cds
u51241cds_717-1029:in_reversesequence,_1257-
1497,eosinophil_eotaxin_receptor_(cmkbr3)_gene,_complete
all_x63755_579-994,mrna_for_high-sulphur_keratin_
5 x80343cds_435-807:in_reversesequence,_1006-
1036,p35_mrna_for_regulatory_subunit_of_cdk5_kinase
all_x83929_2707-3257,mrna_for_typedesmocollin_

Metagene 280
10
u60665_1603-2149,testis_specific_basic_protein_(tsbp),_complete_cds

Metagene 248

15 m16474mrna_1788-2223,fetal_butrylcholinesterase_mrna,_complete_cds
u25433_2428-
2842:not_in_gb_record,protein_associated_with_tumorigenic_conversion_(catr1.3)_mrna,_com
u59423_1481-1943,smad1_mrna,_complete_cds
x76538_433-931,mpv17_mrna

20
Metagene 416

all_m16404_1576-2153,m2_muscarinic_acetylcholine_receptor_gene_
m73746_2409-2894,lutropin/choriogonadotropin_receptor_(lhgr)_mrna,_complete_cds

25
Metagene 3

j00117mrna_9-428,chorionic_gonadotropin_(hcg)_beta_subunit_mrna,_complete_cds
m12759cds_65-335:in_reversesequence,_1020-1260,ig_j_chain_gene
30 all_m85220_15-
201,heavy_chain_disease_iga_chain_gene,_ch3_region_with_a_369_bp_deletion,_3'_end
s71043mrna_442-
970,_ig_alpha_2=immunoglobulin_a_heavy_chain_allotype(constant_region,_germ_line)}_[hu
u24152_1879-2215,p21-activated_protein_kinase_(pak1)_gene,_complete_cds

35 all_x60992_2450-3021,cd6_mrna_for_t_cell_glycoprotein_cd6

Metagene 472

h46990_40-

355, yo16d02.slcdna_clone_178083_3'_similar_to_gb:j02625_cytochrome_p450_1ie1_(human);
m86873mrna_155-367,type_a_plasminogen_related_gene_
s42303_3537-4029,_n-cadherin_[human,_umbilical_vein_endothelial_cells,_mrna,_4132_nt]_
5 all_z80776_596-795,h2a/g_gene

Metagene 457

- 10 d10202_1209-1557,mrna_for_platelet-activating_factor_receptor,_complete_cds
d13643_3585-4131,mrna_for_kiaa0018_gene,_complete_cds
d49387_401-917,mrna_for_nadp_dependent_leukotriene_b4_12-
hydroxydehydrogenase,_partial_cds/gb=d49387
hg4606-ht5011_at_hg4606-ht5011_centractin,_alpha_
j03890mrna#1_482-1022:not_in_gb_record,_sp-cl_gene_(pulmonary_surfactant_protein_sp-
15 c)_extracted_fro
k03195_2303-2813,(hepg2)_glucose_transporter_gene_mrna,_complete_cds_
113210_1668-2214,mac-2_binding_protein_mrna,_complete_cds
120348exon_15-219:not_in_gb_record,oncomodulin_gene
142563mrna_3011-3443,(clone_lsw34)_non-gastric_h,k-atpase_(atp1a1)_gene
20 m27504_2078-2626,topoisomerase_type_ii_(topo_ii)_mrna,_partial_cds/gb=m27504_/ntype=rna_
m28215_130-676,gtp-binding_protein_(rab5)_mrna,_complete_cds
u20648_316-766,zinc_finger_protein_(znf154)_mrna,_partial_cds
y00318cds#1_1317-1653:in_reversesequence,_1814-
1916,mrna_for_complement_control_protein_factor_i
25 all_z15108_1535-2130,mrna_for_protein_kinase_c_zeta

Metagene 443

- 30 ab000468_2302-2860,mrna_for_zinc_finger_protein,_clone_res4-26,_complete_cds_
ab002533_1726-2128,mrna_for_qip1,_complete_cds_
reverse_ac002077_3475-3730,cosmid_clone_luca17_from_3p21.3_
ad000092cds#2_714-1008:in_fullsequence,_87557-87797,_hypotheticalserine-
threonine_protein_kinase_r31
d16480_2089-2641,mrna_for_mitochondrial_enoyl-coa_hydratase/3-hydroxyacyl-
35 coa_dehydrogenase_alpha-su
d38552_1532-2012,mrna_for_kiaa0073_gene,_partial_cds_
d63475_1309-1819,mrna_for_kiaa0109_gene,_complete_cds
d63477_4745-5243,mrna_for_kiaa0143_gene,_partial_cds_
d79206exon#5_1513-2053,gene_for_ryudocan_core_protein,_exon1-5,_complete_cds_

- d85245_1248-1806,mrna_for_tr3beta_complete_cds
all_d87017_16956-
20256_c7_segment_gene_extracted_from(lambda)_dna_for_immunoglobulin_light_chain_
d87116_1514-2048,mrna_for_map_kinase_kinase_3b_complete_cds_
- 5** hg2290-ht2386_at_hg2290-ht2386_calcitonin
hg2755-ht2862_at_hg2755-ht2862_t-plastin_
hg2887-ht3031_at_hg2887-ht3031_sry-related_hmg-boxprotein
hg331-ht331_at_hg331-ht331_tenascin
hg3897-ht4167_at_hg3897-ht4167_sodium_channel_type_iii_alpha_subunit_brain
- 10** hg3925-ht4195_s_at_hg3925-ht4195_surfactant_protein_sp-a2_delta_
j02906mrna_1254-1782,cytochrome_p450iifl_protein(cyp2f)_mrna_complete_cds_
l25444_2124-2694,(tafi70-alpha)_mrna_complete_cds_
m22960mrna_1352-1760,protective_protein_mrna_complete_cds_
m24439exon_492-912,liver/bone/kidney-type_alkaline_phosphatase(alpl)_gene_
15 m60284cds_835-1144:in_reversesequence_251-479,neurokinin_a_receptor(nk-2r)_gene_
m68941mrna_3078-3618,protein-tyrosine_phosphatase_mrna_complete_cds_
m91669_4061-4636,bullous_pemphigoid_autoantigen_bp180_gene_3'_end_
m92303_3057-3633,voltage-dependent_calcium_channel_beta-1_subunit_mrna_complete_cds_
m95623exon#14-15_2-
20 383:not_in_gb_record_pbpd_gene(hydroxymethylbilane_synthase)_extracted_fromhydr
s38742_1370-1835_hox11=hox11_homeodomain{homeobox}[human_mrna_1988_nt]
s65583mrna_588-1068_sp-10=intracrosomal_protein{alternatively_spliced}[human_liver_genomic_2
s87759_1823-2321_protein_phosphatase_2c_alpha[human_teratocarcinoma_mrna_2346_nt]
25 u01337exon#16_412-553,ser/thr_protein_kinase(a-raf-1)_gene_complete_cds_
u04898_1421-1877,orphan_hormone_nuclear_receptor_roralpha2_mrna_complete_cds_
u11292_2353-2863,ki_nuclear_autoantigen_mrna_complete_cds_
u15655_2102-2576,ets_domain_protein_erb_mrna_complete_cds_
u25034_588-1127,neuronatin_beta_mrna_complete_cds_
30 u25956mrna_1470-2046,p-selectin_glycoprotein_ligand(selplg)_gene_
u30894_2068-2626,n-sulphoglucosamine_sulphohydrolase_mrna_complete_cds_
u32439_1324-1822,regulator_of_g-protein_signaling_similarity(rgs7)_mrna_partial_cds_
u32674cds_593-1060:in_reversesequence_1181-
1191,orphan_receptor_gpr9(gpr9)_gene_partial_cds_
35 u39573_2173-2689,salivary_peroxidase_mrna_complete_cds_
u40391mrna_464-980,serotonin_n-acetyltransferase_gene_complete_cds_
u40434_1561-2071,mesothelin_or_cak1_antigen_precursor_mrna_complete_cds_
u42031_1655-2201,54_kda_progesterone_receptor-associated_immunophilin_fkbp54_mrna_partial_cds_

- u43374_775-1069,normal_keratinocyte_mrna_
u45973_1634-2192,phosphatidylinositol_(4,5)bisphosphate_5-
phosphatase_homolog_mrna,_partial_cds
u46751_1562-
- 5** 2012,phosphotyrosine_independent_ligand_p62_for_the_lck_sh2_domain_mrna,_complete_cds
u49857_314-749,transcriptional_activator_mrna,_complete_cds
u50330_3071-3515,procollagen_c-proteinase_(pcp-2)_mrna,_complete_cds_
u68111mrna_858-1374,protein_phosphatase_inhibitor(ppp1r2)_gene
u70671_695-1115,ataxin-2_related_protein_mrna,_partial_cds_
- 10** u72206_3122-3590,guanine_nucleotide_regulatory_factor_(lfp40)_mrna,_complete_cds_
u92457_2832-3375,metabotropic_glutamate_receptormrna,_complete_cds
x05855cds_12-65:not_in_gb_record,histone_h3.3_gene_exon_2,histone_h3.3_gene_exon_2_
all_x07290_1212-1723,hf.12_gene_mrna_
all_x07767_1948-2516,mrna_for_camp-
- 15** dependent_protein_kinase_catalytic_subunit_type_alpha_(ec_2.7.1.3
all_x07948_3-428,mrna_for_transition_protein(tp1)_
x59932mrna_1557-2063,mrna_for_c-src-kinase_
all_x66945_3582-3931,n-sam_mrna_for_fibroblast_growth_factor_receptor
x78687exon#6_172-670,g9_gene_encoding_sialidase
- 20** x79865cds_267-411:in_reversesequence,_922,mrp17_mrna
x81372cds_701-791:in_reversesequence,_1027-1195,mrna_for_biphenyl_hydrolase-related_protein
all_x89066_3817-4019,mrna_for_trpc1_protein
all_x91504_970-1523,mrna_for_arpl_protein
all_x94232_2035-2528,mrna_for_novel_t-cell_activation_protein
- 25** all_x98482_45-
72,tnnt2_gene_exon/gb=x98482_/ntype=dna_/annot=mrna,tnnt2_gene_exon/gb=x98482_/ntype=d
all_z12962_31-398,mrna_for_homologue_to_yeast_ribosomal_protein_l41
z22548cds_310-547:in_reversesequence,_684-894,thiol-specific_antioxidant_protein_mrna_
z73497cds_28-
- 30** 229,dna_sequence_from_cosmid_u240c2,_between_markers_dxs366_and_dxs87_on_chromosome_x
co
- Metagene 430
- 35** d87458_3244-3784,mrna_for_kiaa0282_gene,_partial_cds_
m99564_2505-2991,(clone_dn10mel)_p_protein_mrna,_complete_cds_
- Metagene 426

- d30037_609-1179,mrna_for_phosphatidylinositol_transfer_protein_(pi-tpbeta),_complete_cds_
 all_j03027_3437-3996,mhc_i_hla-6.09_gene,_complete_cds_
 all_m14306_171-361,beta-a3/a1-crystallin_gene_(hu-beta-a3/a1)
 all_m30703_55-142:not_in_gb_record,amphiregulin_(ar)_gene_
5 u14407_601-1147,interleukin(il15)_mrna,_complete_cds_
 u33054_1584-2010,g_protein-
 coupled_receptor_kinase_grk4_mrna,_alpha_splice_variant,_complete_cds_
 x94629_618-1128,mrna_for_metaphase_chromosomal_protein
 y10518mrna_138-648,mrna_for_cd202_protein/gb=y10518_/ntype=ma_
10 z83804_29-261,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc7).
- Metagene 406
- u06454_1832-2288,amp-activated_protein_kinase_(hampk)_mrna,_complete_cds_
15 all_y00705_5-356,psti_mrna_for_pancreatic_secretory_inhibitor_(expressed_in_neoplastic_tissue).
- Metagene 393
- j03474cds_3-255,serum_amyloid_a_gene,_complete_cds_
20 all_m63262_161-540:in_m63262cds_231-340,5-lipoxygenase_activating_protein_(flap)_gene_
 all_x51441_55-90,mrna_for_serum_amyloid_a_(saa)_protein_partial,_clone_pas3-
 alpha,mrna_for_serum_amy
 x75042cds_1607-1817:in_reversesequence,_2024-2252,rel_proto-oncogene_mrna_
25 Metagene 381
- af005361_1159-1663,importin_alphamrna,_complete_cds/gb=af005361_/ntype=rna_
 hg3731-ht4001_r_at_hg3731-ht4001_immunoglobulin_heavy_chain,_vdjrc_regions_
 l38616mrna_1184-1634,brain_and_reproductive_organ-
30 expressed_protein_(bre)_gene,_complete_cds
 u46746_1183-1708,dystrobrevin-epsilon_mrna,_complete_cds_
 all_u61500_6060-6577,gt334_protein_(gt334)_gene_mrna,_complete_cds_
 Metagene 361
35
- m16364_749-1311,creatine_kinase-b_mrna,_complete_cds_
 m64554mrna_1602-
 1962,_f13a1_gene_(coagulation_factor_xiiib)_extracted_fromfactor_xiii_b_subunit_gene
 u07794_cds2_at_u07794_u07794,not_in_gb_record,tyrosine_kinase_(tkk)_gene

Metagene 357

- hg3432-ht3620_s_at_hg3432-ht3620_fibroblast_growth_factor_receptor_k-sam, altsplice_3, k-
5 sam_iii_
 s79048_61-421, lprp=phl_elfl [human, lacrimal_gland, mrna_partial, 507_nt]
 u39657_2341-2863, map_kinase_kinase(mkk6)_mrna, complete_cds_
 u97188_3602-4010, putative_rna_binding_protein_koc_(koc)_mrna, complete_cds
 x66417cds_230-524:in_reversesequence, 658-766, cask_mrna_for_kappa-casein

10

Metagene 354

- aj000480cds_116-650, mrna_for_c8fw_phosphoprotein/gb=aj000480_/ntype=rna_
 d21241exon#2_2-72, ovary_and_prostate-specific_exonfromcytochrome_p-
15 450_aromatase_gene, multiple_ex
 d30742_1211-1697, mrna_for_calmodulin-dependent_protein_kinase_iv, complete_cds_
 d80011_4259-4793, mrna_for_kiaa0189_gene, complete_cds
 hg1980-ht2023_at_hg1980-ht2023_tubulin_beta_2_
 hg2264-ht2360_at_hg2264-ht2360_atpase_ca2+_transporting_plasma_membrane_1, altsplice_6_
20 hg273-ht273_at_hg273-ht273_lymphocyte_antigen_hla-g3_
 hg3517-ht3711_at_hg3517-ht3711_alpha-1-antitrypsin_5'_end_
 hg620-ht620_at_hg620-ht620_tyrosine_phosphatase_epsilon_
 l05424_cds2_at_l05424_l05424, not_in_gb_record, cd44_gene_(cell_surface_glycoprotein_cd44)_ex-
 tracted_
25 l10844_1646-2213, cellular_growth-regulating_protein_mrna, complete_cds_
 l14848_802-1181, mhc_i-related_protein_mrna, complete_cds_
 l28957_685-1231, ctp:phosphocholine_cytidyltransferase_mrna, complete_cds
 all_m23178_2889-3818, homologue-
 l_of_gene_encoding_alpha_subunit_of_murine_cytokine_(mip1/sci), compl
30 m27436mrna_1638-
 l979, tissue_factor_gene, complete_cds, with_a_alu_repetitive_sequence_in_the_3'_untr
 m27819_3060-3426, anion_exchange_protein(ae1_band_3)_mrna, complete_cds_
 m33318mrna_1538-1583, cytochrome_p450iia3_(cyp2a3)_mrna, complete_cds_
 m62324_1584-2052, modulator_recognition_factor_i_(mrf-1)_mrna, 3'_end_
35 u30888_1892-2420, trna-guanine_transglycosylase_mrna, complete_cds
 u40571_1695-2073, alpha1-syntrophin_(snt_a1)_mrna, complete_cds_
 u82310_19-229, unknown_protein_mrna, partial_cds/gb=u82310_/ntype=rna_
 u82818_1005-1058, ucp3s_mrna, complete_cds/gb=u82818_/ntype=rna
 u84551_cds2_at_u84551_u84551, not_in_gb_record, dystrobrevin_(dm)_gene_

- x03934cds_255-423:in_reversesequence, 3890-4112,t-cell_antigen_receptor_gene_t3-delta_
all_x07619_658-1162,mrna_for_cytochrome_p450_db1_variant_b_
x12458mrna_1566-2046, p3_protein (aa_1-1382)_gene_extracted_fromp3_gene_
all_x13967_3247-3806,mrna_for_leukaemia_inhibitory_factor_(lif/hilda)
- 5** x16901cds_411-711:in_reversesequence, 866-
1094,mrna_for_rap30_subunit_of_transcription_initiation_fa
x52599cds_295-649,mrna_for_beta_nerve_growth_factor
x94563mrna#1_109-
123, exon_1b;_used_only_in_typetranscripts_fromdbi/acbp_gene_exon&/gb=x94563_/ntype
- 10** y10506mrna_251-593,mrna_for_cd110_protein/gb=y10506_/ntype=rna_
y10615cds_115-535,cym2_gene/gb=y10615_/ntype=dna_/annot=cds_
all_z46632_2953-3206,hspde4c1_gene_for_3',5'-
cyclic_AMP_phosphodiesterase,hspde4c1_gene_for_3',5'
- 15** Metagene 346
- u45974_1007-1517,phosphatidylinositol_(4,5)_bisphosphate_5-
phosphatase_homolog_mrna, partial_cds_
u79304_1102-1630,clone_23909_mrna, partial_cds.
- 20** x05839mrna_2298-
2467, transforming_growth_factor_beta precursor_gene_extracted_fromtransforming_growt
- Metagene 340
- 25** l34838_40-586,early_placenta_insulin-like_peptide_epil_(insl4)_mrna, complete_cds_
all_u05255_159-188,glycophorin_hep2_mrna, partial_cds, glycophorin_hep2_mrna, partial_cds
u31501_2359-
2773,fragile_x_mental_retardation_syndrome_related_protein_(fmr2)_mrna, complete_cds_
u37689_344-752,rna_polymerase_ii_subunit_(hsrpb8)_mrna, complete_cds_
- 30** x15943mrna_884-1220:in_reversesequence, 7046-7076, huamn_calcitonin/alpha-cgrp_gene
- Metagene 336
- u08021_447-909,nicotinamide_n-methyltransferase_(nnmt)_mrna, complete_cds
- 35** all_x83107_1867-2348,bmx_mrna_for_cytoplasmic_tyrosine_kinase
- Metagene 333

- u96191_19-439,trophoblast_hypoxia-regulated_factor-5_(hrf-5)_mna,_3'_end/gb=u96191_/ntype=rna_
all_x13955_675-827,mrna_for_myosin_alkali_light_chain
x64877cds_417-762:in_reversesequence,_889-
- 5** 894,mrna_for_serum_protein,mrna_for_serum_protein
- Metagene 322
- hg2229-ht2306_at_hg2229-ht2306_paired_box_hup1_
10 m54914exon_1099-1666,follicle-stimulating_hormone_beta-subunit_gene
- Metagene 267
- hg544-ht544_at_hg544-ht544_endothelial_cell_growth_factor_
15 105072exon#10_375-907,interferon_regulatory_factorgene,_complete_cds_
107261mrna_283-
505,alpha_adducin_mrna,_partial_cds_including_alterate_exons_a_and_b_(trimmed_to_889
137360_146-698,(clone_hehk1-1)_ehk1_receptor_tyrosine_kinase_ligand_(efl-2)_mrna,_complete_cds
- 20** 177567mrna_947-1231,mitochondrial_citrate_transport_protein(ctp)_mrna,_3'_end
m25667_1086-1200,neuronal_growth_protein_43_(gap-43)_mrna,_complete_cds
m32886_351-843,sorcin_cp-22_mrna,_complete_cds_
u07151_395-869,gtp_binding_protein(arl3)_mrna,_complete_cds_
u29175_5199-5223,transcriptional_activator(brg1)_mrna,_complete_cds.
- 25** u30827_1253-1817,splicing_factor_srp40-3_(srp40)_mrna,_complete_cds
u30999_25-379,(memc)_mrna,_3'_utr/gb=u30999_/ntype=rna_
u51432_1557-2079,nuclear_protein_skip_mrna,_complete_cds.
u53830_1469-1835,interferon_regulatory_factor_7a_mrna,_complete_cds_
u60873_115-439,clone_137308_mrna,_partial_cds
- 30** u79261_883-1422,clone_23959_mrna,_partial_cds
all_x14813_1077-1618,liver_mrna_for_3-oxoacyl-coa_thiolase_
x64177cds_8-147:in_reversesequence,_2-277,mrna_for_metallothionein
x94333_1617-2157,mrna_for_tgn46_protein
x97074cds_182-398:in_reversesequence,_704-782,mrns_for_clathrin-associated_protein
- 35** z46376mrna_4703-5249,hk2_mrna_for_hexokinase_ii_

Metagene 264

d21239_3475-3997,mrna_for_c3g_protein,_complete_cds

- d49958_1830-2346,fetus_brain_mrna_for_membrane_glycoprotein_m6,_complete_cds_
d88613_1068-1518,mrna_for_hgcma,_complete_cds
d88667_1298-1652,mrna_for_cerebroside_sulfotransferase,_complete_cds_
hg1098-ht1098_at_hg1098-ht1098_cystatin_d
- 5** hg2161-ht2231_at_hg2161-ht2231_translocation-associated_notch_(drosophila)_homolog
hg2191-ht2261_at_hg2191-ht2261_crystallin,_beta_b3_
hg3477-ht3670_at_hg3477-ht3670_cd4_antigen_
hg3928-ht4198_at_hg3928-ht4198_surfactant_protein_sp-a1_delta_
hg4336-ht4606_at_hg4336-ht4606_bactericidal_bpi'gene_
- 10** hg4535-ht4940_s_at_hg4535-ht4940_dematin_
j02888_453-915,quinone_oxidoreductase_(nqo2)_mrna,_complete_cds
k03008cds_90-118:not_in_gb_record,_gamma-g2-psi_gene_extracted_fromgamma-c-
crystallin_(gamma-3)_gene
111372_497-893,protocadherin_43_mrna,_3'_end_of_cds_for_alternative_splicing_pc43-12_
- 15** 117327_16-196,pre-t/nk_cell_associated_protein_(3b3)_mrna,_3'_end
140904mrna_1228-
1656,_hsapiens_peroxisome_proliferator_activated_receptor_gamma,_complete_cds_
m12625mrna_893-1259:in_reversesequence,_1599-1683,lecithin-
cholesterol_acyltransferase_mrna,_complet
- 20** m14123cds#1_263-665,_pol_fromendogenous_retrovirus_herv-
k10/gb=m14123_/ntype=dna_/annot=cds,_pol_fro
all_m16707_590-
631,histone_h4_gene,_complete_cds,_clone_fo108,histone_h4_gene,_complete_cds,_clone_f
m21302_402-514,small_proline_rich_protein_(sprii)_mrna,_clone_174n_
- 25** m21904cds_1189-1549:in_reversesequence,_372-
378,4f2_glycosylated_heavy_chain_(4f2hc)_antigen_gene_
m61733_2454-2934,erythroid_membrane_protein_4.1_mrna,_complete_cds
m90366_1683-2175,zona_pellucida_glycoprotein(zp2)_mrna,_complete_cds
m91585_3719-4175,br140_mrna,_complete_cds
- 30** s80267_1304-1872,_p72syk_{g_insertion_nucleotide_92}_{human,_jurkat_e6-
l_j.cam1_cells,_mrna_partial_
u01120_2484-2982,glucose-6-phosphatase_mrna,_complete_cds
u04270_3505-3973,putative_potassium_channel_subunit_(h-erg)_mrna,_complete_cds_
u07856cds#5_1300-1846,endogenous_retrovirus_in_complement_c4a_gene,_a3_allele,_herv-
k(c4)_(gag),_(po
- 35** u11090_733-1243,hydroxyindole-o-methyltransferase_promoter_a-
derived_(hiomt)_mrna,_complete_cds
u13666cds_671-989:in_reversesequence,_1329-1413,g_protein-
coupled_receptor_(gpr1)_gene,_complete_cds

- u18244_1166-1640,excitatory_amino_acid_transportermrna,_complete_cds
u18543_1853-2339,zinc-finger_protein_mrna,_complete_cds
all_u19107_3423-3658,znf127_(znf127)_gene,_complete_cds_
u19977_735-1227,preprocarboxypeptidase_a2_(procpa2)_mrna,_complete_cds_
5 u20582_1180-1690,actin-like_peptide_mrna,_partial_cds
u20657_2439-2890:not_in_gb_record,ubiquitin_protease_(unph)_proto-
oncogene_mrna,_complete_cds_
u31342mrna_1173-1629,nucleobindin_gene_
u33317mrna_25-421,defensin(hd-6)_gene,_complete_cds
10 u33761_1017-1557,cyclin_a/cdk2-associated_p45_(skp2)_mrna,_complete_cds
u36501_1704-2148,sp100-b_(sp100-b)_mrna,_complete_cds
u43148_6015-6483,patched_homolog_(ptc)_mrna,_complete_cds
u48263_627-1173,pre-pro-orphanin_fq_(ofq)_mrna,_complete_cds_
u49973cds#1_764-
15 1340,orf1;_mer37;_putative_transposase_similar_to_pogo_element_fromtiger1_transpos
u59878_469-895,low-mr_gtp-binding_protein_(rab32)_mrna,_partial_cds
u76010_1520-1964,putative_zinc_transporter_znt-3_(znt-3)_mrna,_complete_cds
u77845_1515-1905,htrip_(htrip)_mrna,_complete_cds
u78793_6-29,folate_receptor_alpha_(hfr)_mrna,_partial_cds/gb=u78793/_ntype=rna_
20 u86759_1374-1856,netrin-2_like_protein_(ntn2l)_mrna,_complete_cds
all_u90543_2501-
2545,butyrophilin_(btf1)_mrna,_complete_cds,butyrophilin_(btf1)_mrna,_complete_cds
u95019_2358-2862,voltage-dependent_calcium_channel_beta-2c_subunit_mrna,_complete_cds
all_x04297_3519-4090,mrna_for_na,k-atpase_alpha-subunit
25 all_x05246_1045-1556,testis-specific_pgk-2_gene_for_phosphoglycerate_kinase_(atp:3-phospho-d-
glycera
all_x53800_377-961,mrna_for_macrophage_inflammatory_protein-2beta_(mip2beta)_
x76942cds_24-420:in_reversesequence,_487-527,mrna_for_72.1_protein
x92518mrna_4077-4127,mrna_for_hmgi-c_protein_
30 x96783mrna_1442-2015,syt_v_gene_(genomic_and_cdna_sequence)_
all_x97058_1042-1565,mrna_for_p2y6_receptor
y08200_1496-2006,mrna_for_rab_geranylgeranyl_transferase,_alpha-subunit
all_z71460_2546-3033,mrna_for_vacuolar-type_h(+)-atpase_115_kda_subunit
35 Metagene 255

d10922_1288-1808,mrna_for_fm1p-related_receptor_(hm63)_
m11567mrna_188-620,angiogenin_gene,_complete_cds,_and_three_alu_repetitive_sequences

Metagene 253

- ab002356_5330-5807,mrna_for_kiaa0358_gene_complete_cds/gb=ab002356/_ntype=rna_
111701_2320-2609,phospholipase_d_mrna_complete_cds
- 5** 142374mrna_1836-2389,pp2a_b56-beta_mrna_complete_cds_
m19508exon#1_2-98,mpo_frommyeloperoxidase_gene_exons_1-
4/gb=m19508/_ntype=dna/_annot=exon_
all_m32879_690-1129,steroid_11-beta-hydroxylase_(cyp11b1)_gene,steroid_11-beta-
hydroxylase_(cyp11b1)
- 10** m81182_2831-3314,peroxisomal_70_kd_membrane_protein_mrna_complete_cds
u25975_1675-1795,serine_kinase_(hpak65)_mrna_partial_cds
u47686_2174-2747,signal_transducer_and_activator_of_transcription_stat5b_mrna_complete_cds
all_u67092_1093-1868:not_in_gb_record,ataxia-
telangiectasia_locus_protein_(atm)_gene_exons_1a_1b_
- 15** all_x16609_6641-7241,mrna_for_ankyrin_(variant_2.1)
x51953exon#1-2_37-
64:not_in_gb_record,ucp_gene_for_uncoupling_protein_exonsand/gb=x51953/_ntype=dna_
all_x52228_1631-2103,mrna_for_secreted_epithelial_tumour_mucin_antigen_
x58528mrna_2689-3193,pmp70_mrna_for_a_peroxisomal_membrane_protein_
20 x95808mrna_5503-
6037,mrna_for_protein_encoded_by_a_candidate_gene_dxs6673e_for_mental_retardation
z11899cds_446-706:in_reversesequence_989-
1074,otf3_mrna_encoding_octamer_binding_protein_3b
z22951mrna_717-1231,of_p65_gene_encoding_p65_subunit_of_transcription_factor_nf-kappab_
25 reverse_z68280_34936-
35175,dna_sequence_from_cosmid_125a3_huntington's_disease_region_chromosome_4

Metagene 172

- 30** m22430_300-732,rasf-a_pla2_mrna_complete_cds
u80669_863-1403,androgen_regulated_homeobox_protein_(nkx3.1)_mrna_complete_cds
z70222cds_3-213:in_reversesequence_25-37,mrna_for_orf_(clone_icrfp507g2490)

Metagene 123

- 35** d90064_1806-2184,cgm6_mrna_for_cd66b_(nca-95)
m87507_751-1177:in_reversesequence_1012-1130_homo_sapien_interleukin-
1_beta_convertase_(il1bce)_mr
m91556_4785-5343,voltage-gated_sodium_channel_mrna_complete_cds.

u82275_1335-1647,immunoglobulin-like_transcriptmrna,_complete_cds_
x15675mrna_1522-1840,ptr7_mrna_for_repetitive_sequence/gb=x15675_/ntype=rna

Metagene 119

5

d00003_1681-1981,liver_cytochrome_p-450_mrna,_complete_cds,liver_cytochrome_p-
450_mrna,_complete_cds
m74047_1878-2316,steroid_5-alpha-reductase(srd5a2)_mrna,_complete_cds_
s53911_2110-

- 10 2584_cd34=glycoprotein_expressed_in_lymphohematopoietic_progenitor_cells_{alternatively
u42360mrna_867-1346,n33_gene
x54867mrna_783-1293,mrna_for_nkg2-a_gene_
x65663cds_83-137,sox-6_mrna/gb=x65663_/ntype=rna_
y11174cds_48-516:in_reversesequence,_600,mrna_for_rp3_gene/gb=y11174_/ntype=rna_

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Metagene 118

- d12620_1535-1965,mrna_for_cytochrome_p-450ltbv_
d38522_3436-3958,mrna_for_kiaa0080_gene,_partial_cds_
20 d63861exon#10_90-656,dna_for_cyclophilin_40,_complete_cds
hg831-ht831_at_hg831-ht831_potassium_channel_
j02883mrna_55-493,colipase_mrna,_complete_cds
l40393mrna_1754-2222,(clone_s171)_mrna,_complete_cds
m94172_6837-7328,n-type_calcium_channel_alpha-1_subunit_mrna,_complete_cds_
25 u05589_877-1453,ribosomal_protein_s1_homolog_mrna,_partial_cds_
u08854_1612-2040,udp_glucuronosyltransferase_precursor_(ugt2b15)_mrna,_complete_cds
u16954_1099-1579,(af1q)_mrna,_complete_cds_
u17327_6523-7081,neuronal_nitric_oxide_synthase_(nos1)_mrna,_complete_cds
u35637_8831-9367,nebulin_mrna,_partial_cds/gb=u35637_/ntype=rna
30 u47926_1546-1996,unknown_protein_b_mrna,_complete_cds
u90546_1301-
1344,butyrophilin_(btf4)_mrna,_complete_cds,butyrophilin_(btf4)_mrna,_complete_cds
x02158mrna_949-1219,gene_for_erythropoietin_
all_x06562_3951-4396,mrna_for_growth_hormone_receptor
35 x14474cds_669-710,mrna_for_microtubule-associated_tau_protein
all_x86400_560-1155,mrna_for_gamma_subunit_of_sodium_potassium_atpase
all_x98176_772-1022,mrna_for_mach-beta-1_protein/gb=x98176_/ntype=rna
z69030cds_838-1186,mrna_for_gammaisoform_of_61kda_regulatory_subunit_of_pp2a

Metagene 112

- j04621mrna_2879-3347,heparan_sulfate_proteoglycan_(hspg)_core_protein,_3'_end
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5 related_14.
all_x51730_4462-5003,mrna_and_promoter_dna_for_progesterone_receptor_

Metagene 89

- 10 hg2139-ht2208_f_at_hg2139-ht2208_beta-1-glycoprotein_1,_pregnancy-specific_
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alpha_(gpib)_gene,_complete_cds,_clon
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gamma2_chain
15 u73167cds#4_1050-1254;in_reversesequence,_13521-
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all_x66276_3221-3734,mrna_for_skeletal_muscle_c-protein

20 Metagene 78

- af005887_1969-
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25 d13370exon#5_193-637,apx_gene_encoding_apex_nuclease,_complete_cds_
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30 j03263_667-1218,lysosome-associated_membrane_glycoprotein_(lamp_a)_mrna,_complete_cds
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pcc)_gene,_partial_cds_(mutant_delta-atc
m34423_1856-2312,beta-galactosidase_(glb1)_mrna,_complete_cds

- m36429_827-1412,transducin_beta-2_subunit_mrna_complete_cds_
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u28963_567-1143,gps2_(gps2)_mrna_complete_cds_
u29171_1340-1742,casein_kinase_i_delta_mrna_complete_cds
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- 15 u72935mrna#1_7752-
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u81802_2557-3043,ptdins_4-kinase_(pi4kb)_mrna_complete_cds
- 20 x54199mrna_2616-3006:in_reversesequence,_3118,mrna_for_gars-airs-gart_
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phosphate_dehydrogenase)_extracted_fromg6pd_gene_for_glu
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- 35 Metagene 58

x02544cds_256-544:in_reversesequence,_688-772,mrna_for_alpha1-
acid_glycoprotein_(orosomuroid)_
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CLAIMS

What is claimed is:

1. A classification tree model incorporating Bayesian analysis for the statistical
5 prediction of binary outcomes.
2. The tree model of claim 1, wherein the prediction of a binary outcome is dependent on the interaction of data comprising at least two predictor variables.
3. The tree model of claim 2, wherein the data arises by case control design such that the number of 0/1 values in the response data is fixed by design.
- 10 4. The tree model of claim 3, such that the case control design assesses association between predictors and binary outcome with nodes of a tree.
5. The tree model of claim 4, such that the Bayesian analysis comprises using sequences of Bayes factor based tests of association to rank and select predictors that define a node split.
- 15 6. The tree model of claim 5, further comprising the forward generation of at least one class of trees with high marginal likelihood, wherein the prediction of said class of trees is conducted using principles of model averaging.
7. The tree model of claim 6, wherein the principle of model averaging comprises the steps of:
20 weighted prediction of a tree by determining its implied posterior probability by a score;
evaluation of the score to exclude unlikely trees;
evaluation of the posterior and predictive distribution at each node and leaf of a tree;
and
25 application of said posterior and predictive distribution to the evaluation of each tree and the averaging of predictions across trees for future predictive cases.
8. The tree model of claim 1 or 2, wherein the binary outcome is a clinical state.
9. The tree model of claim 1 or 2, wherein the binary outcome is a physiological state.
- 30 10. The tree model of claim 1 or 2, wherein the binary outcome is a physical state.
11. The tree model of claim 1 or 2, wherein the binary outcome is a disease state.

12. The tree model of claim 1 or 2, wherein the binary outcome is a risk group.
13. The tree model of claim 1 or 2, wherein the data is biological data.
14. The tree model of claim 1 or 2, wherein the data is statistical data.

Figure 1

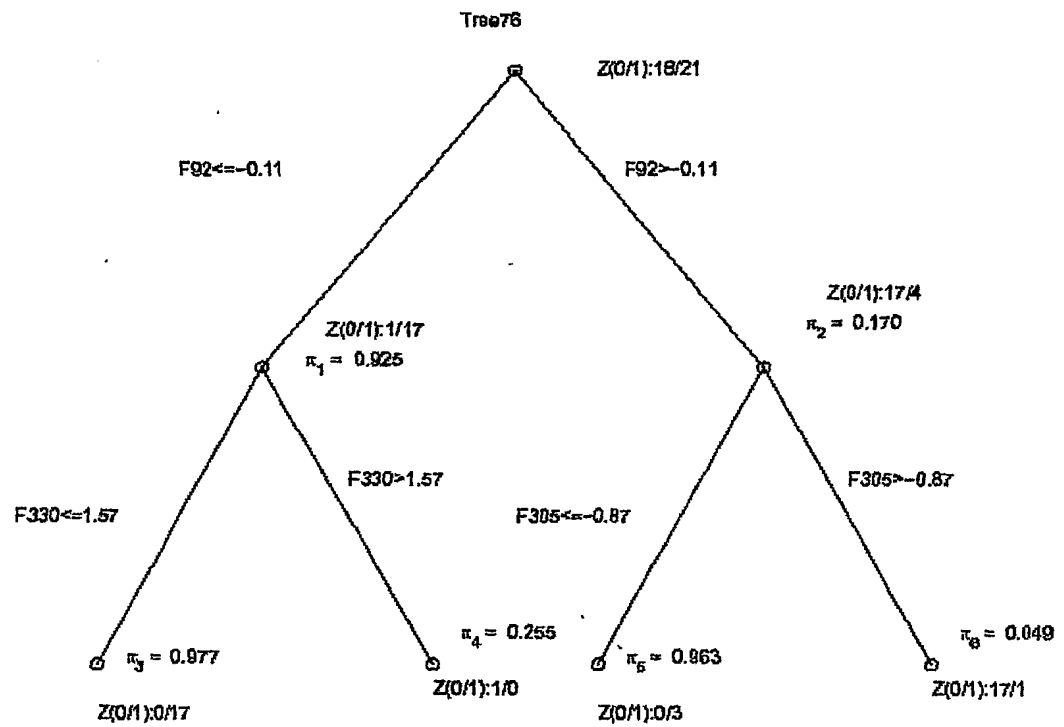


Figure 2

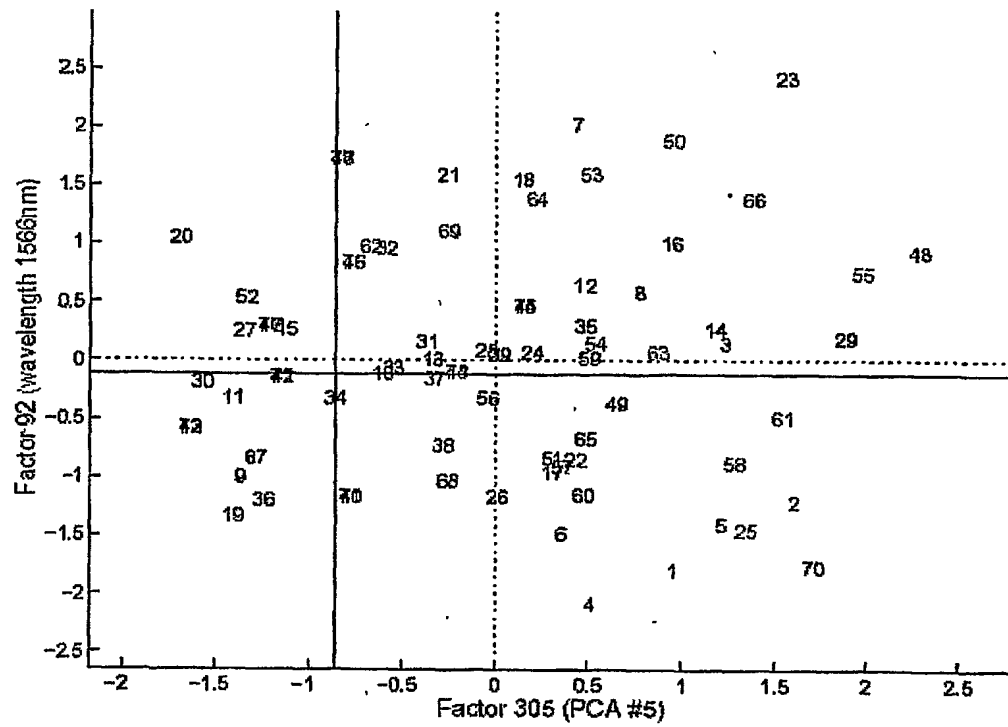


Figure 3

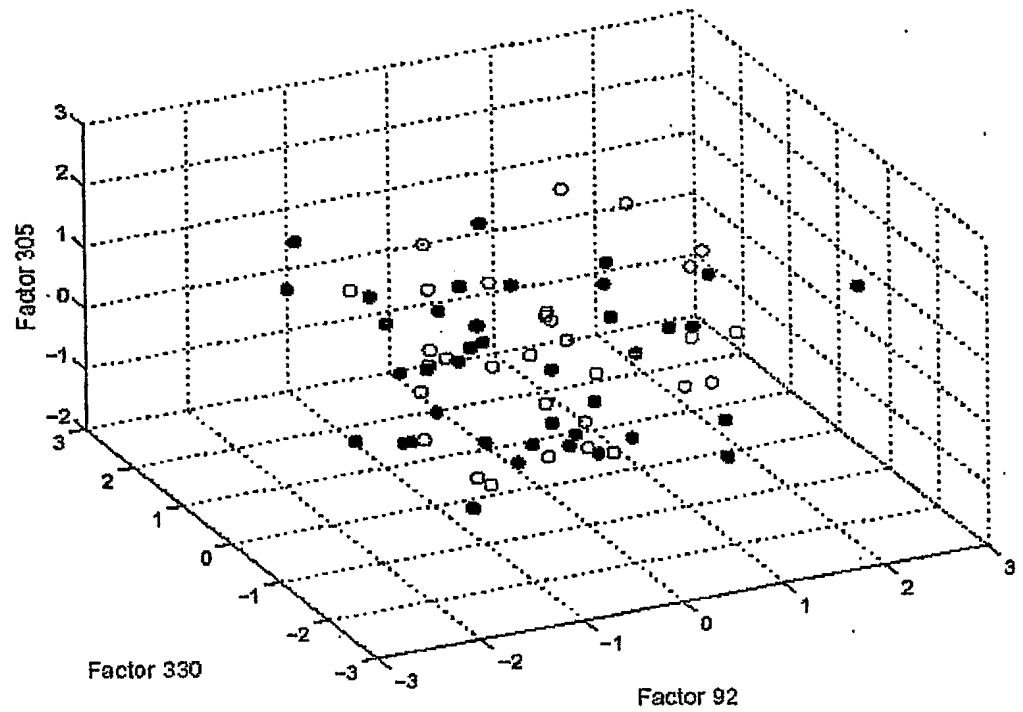


Figure 4

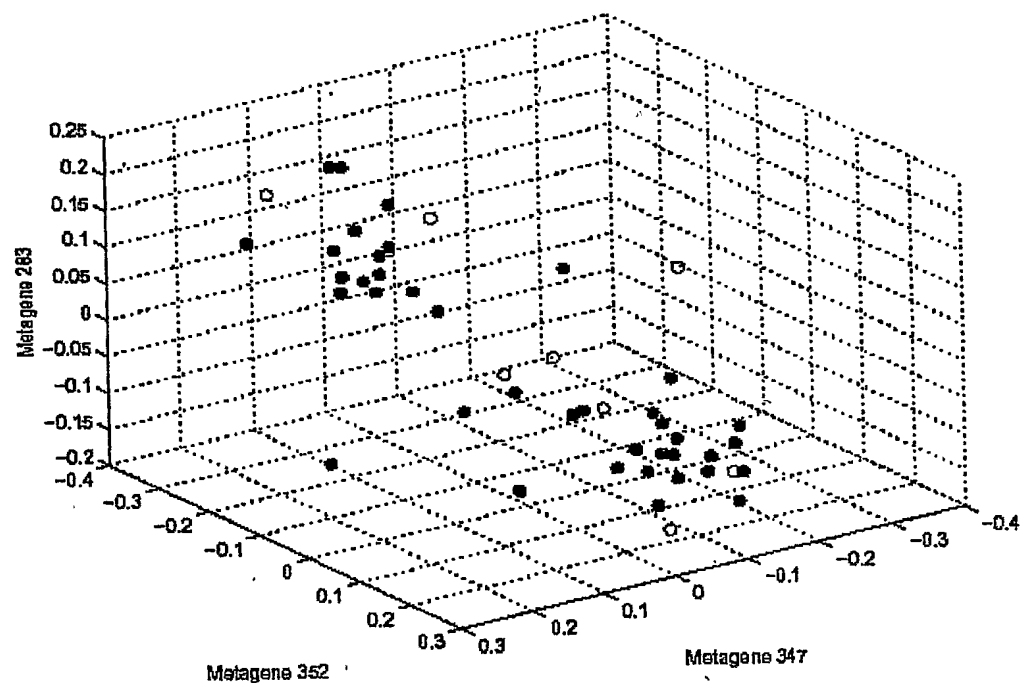


Figure 5

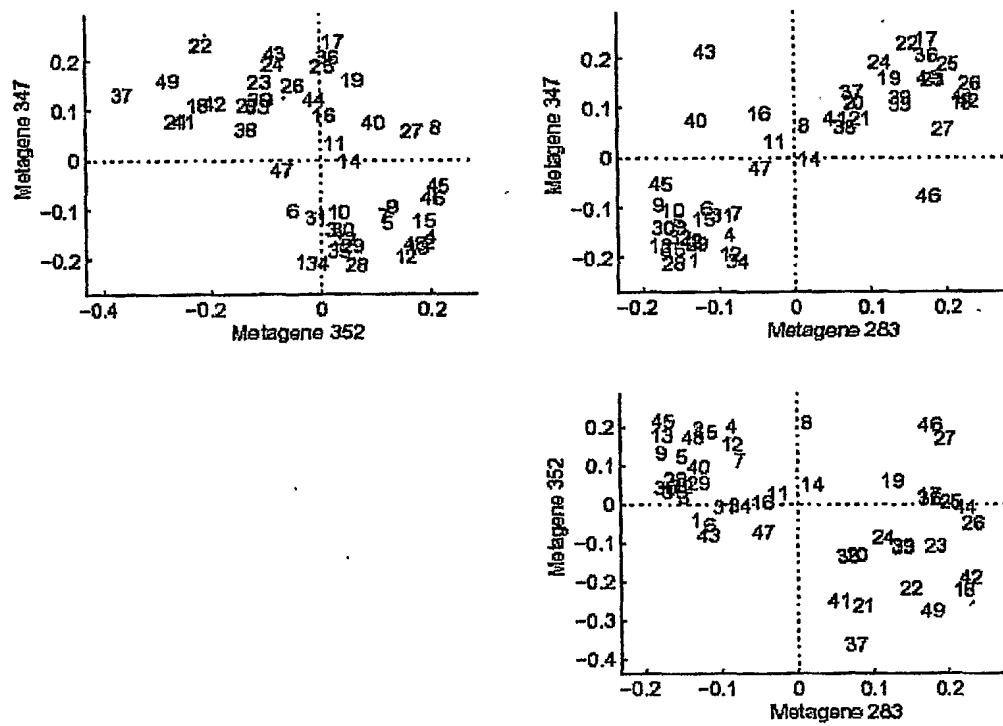


Figure 6

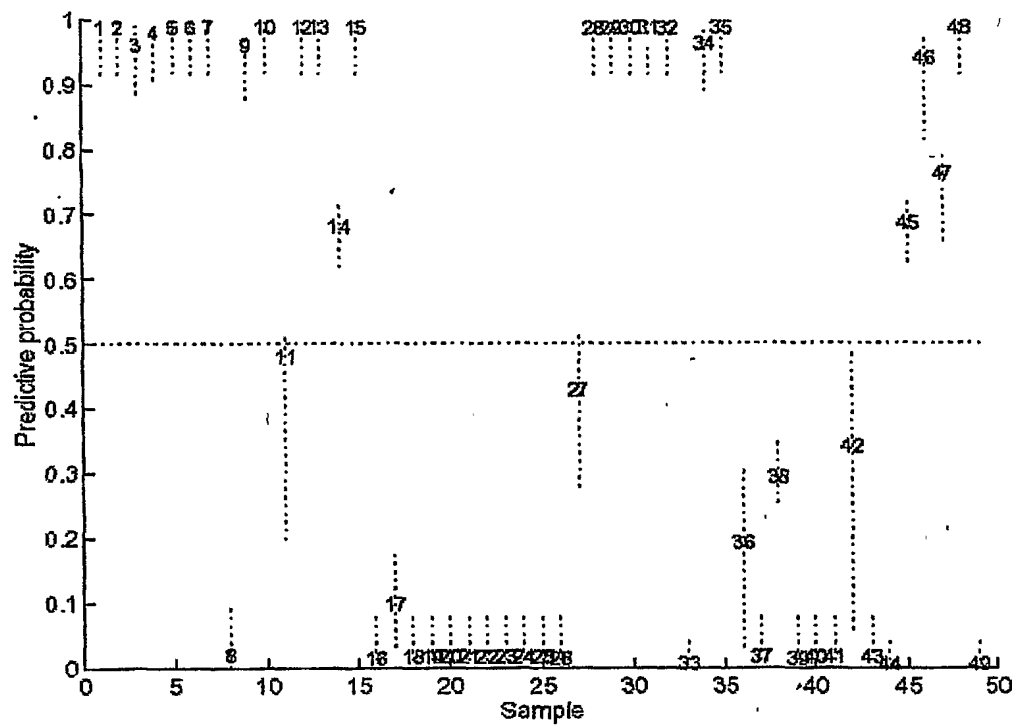


Figure 7

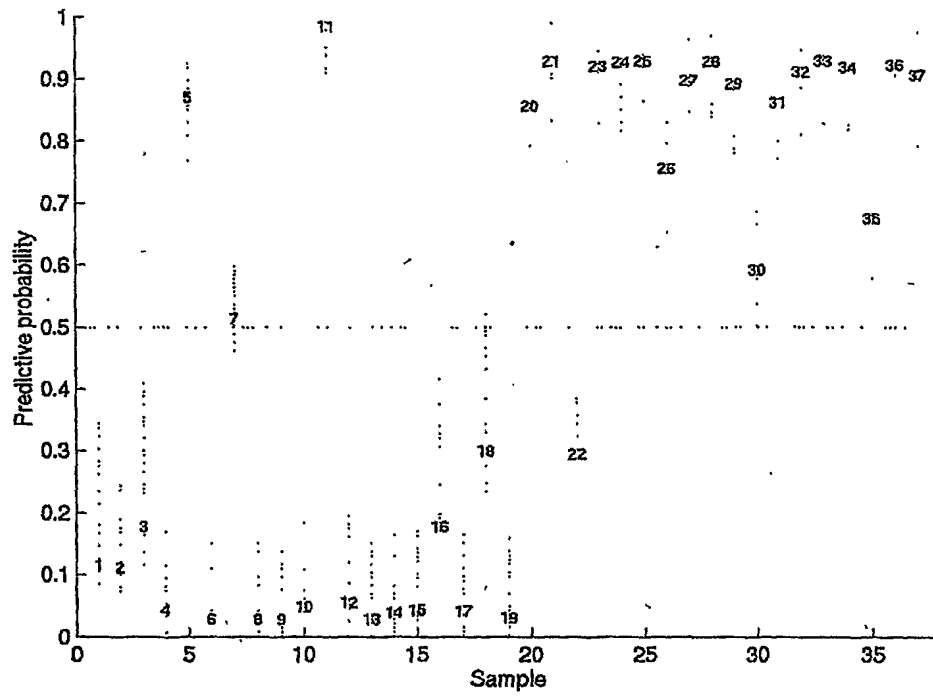


Figure 8

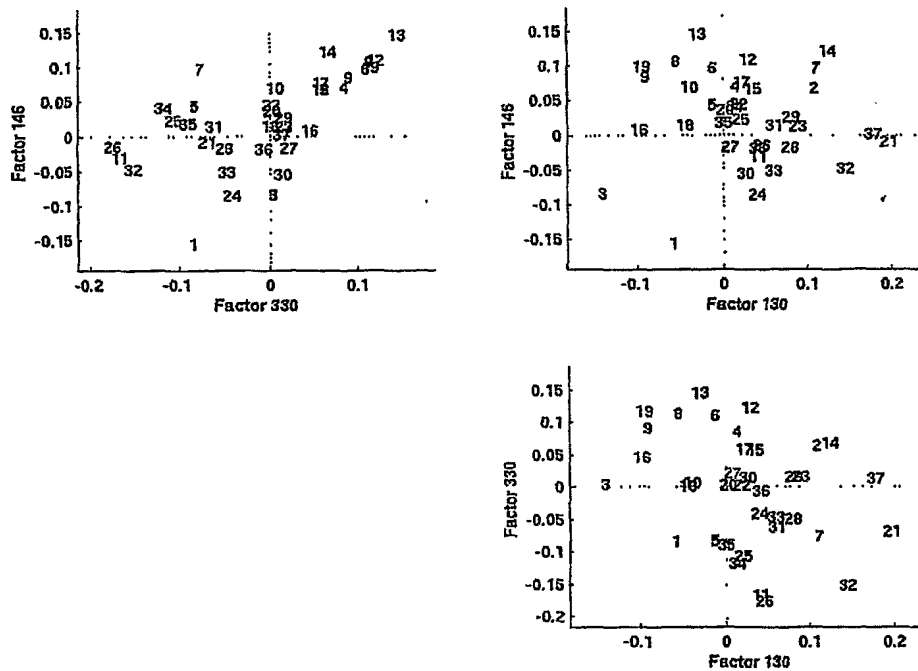


Figure 9

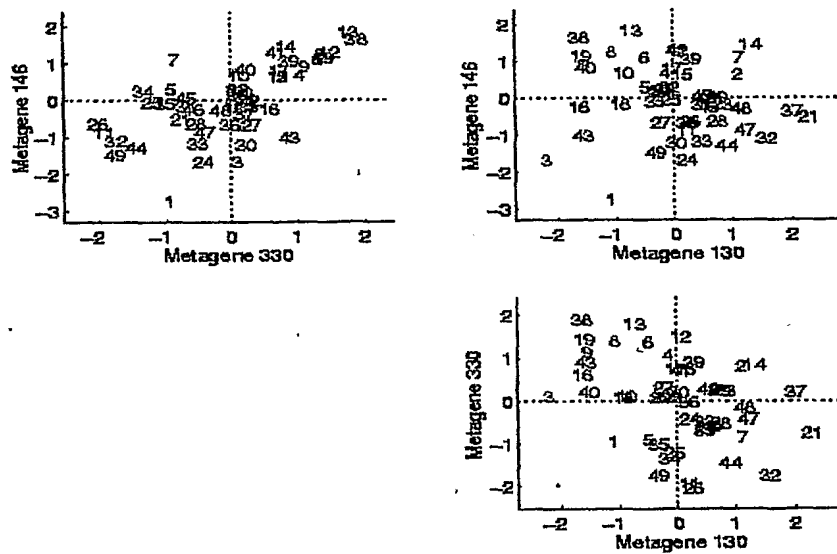
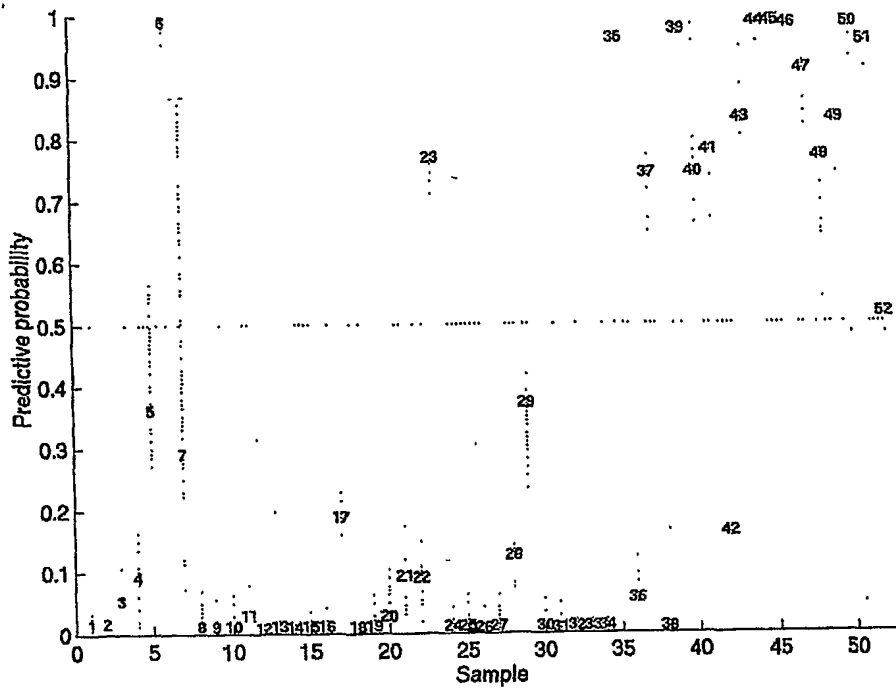


FIG. 10



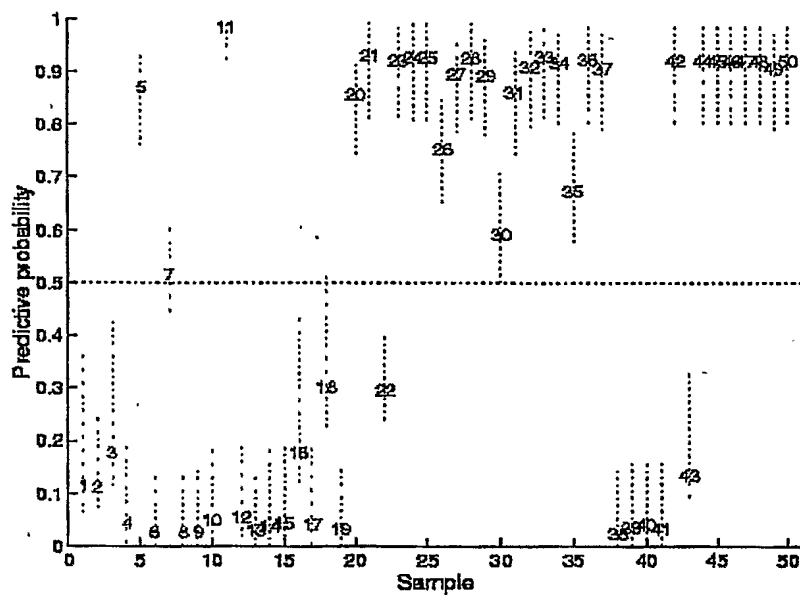


Figure 11

FIGURE 12.

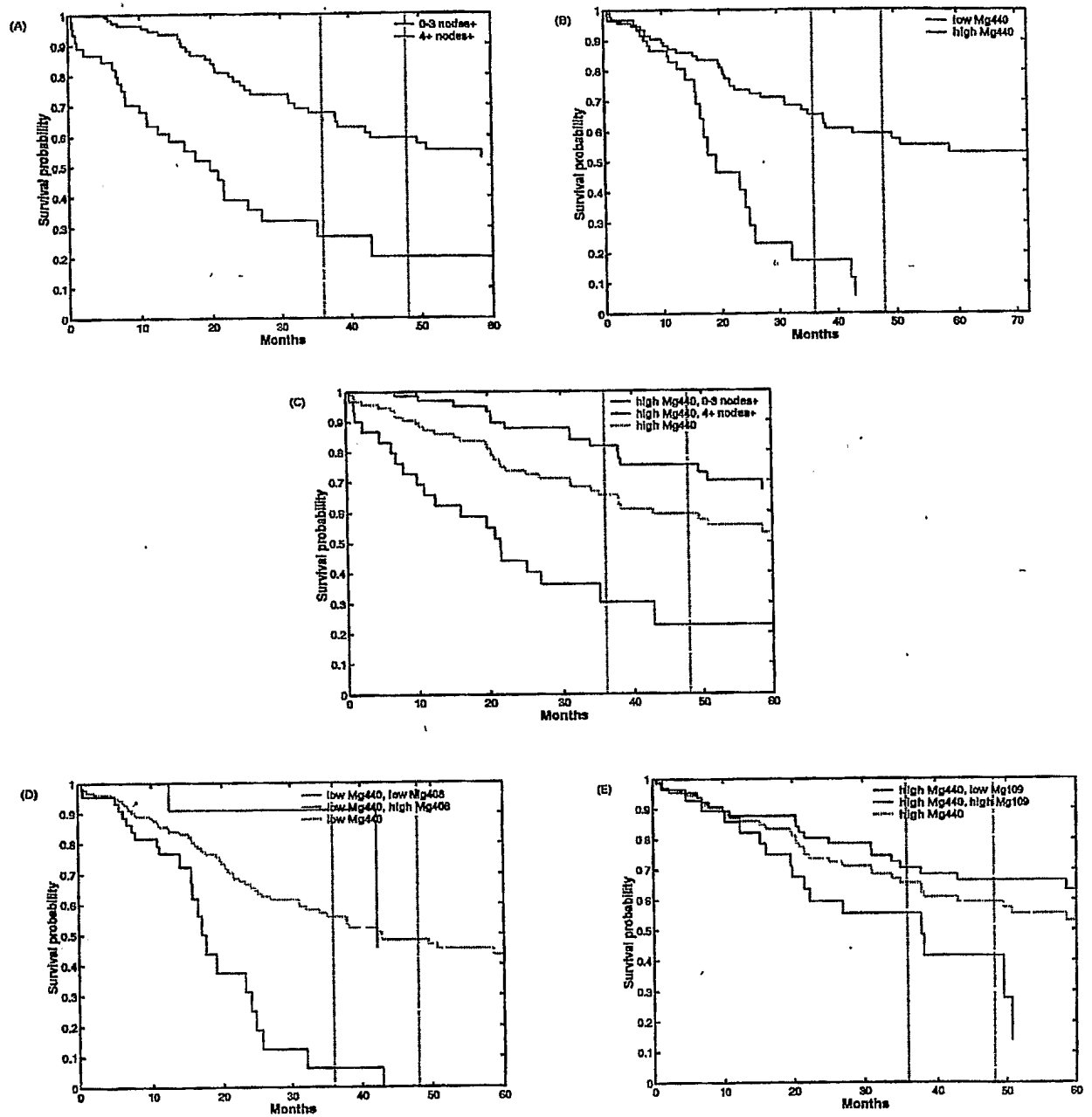
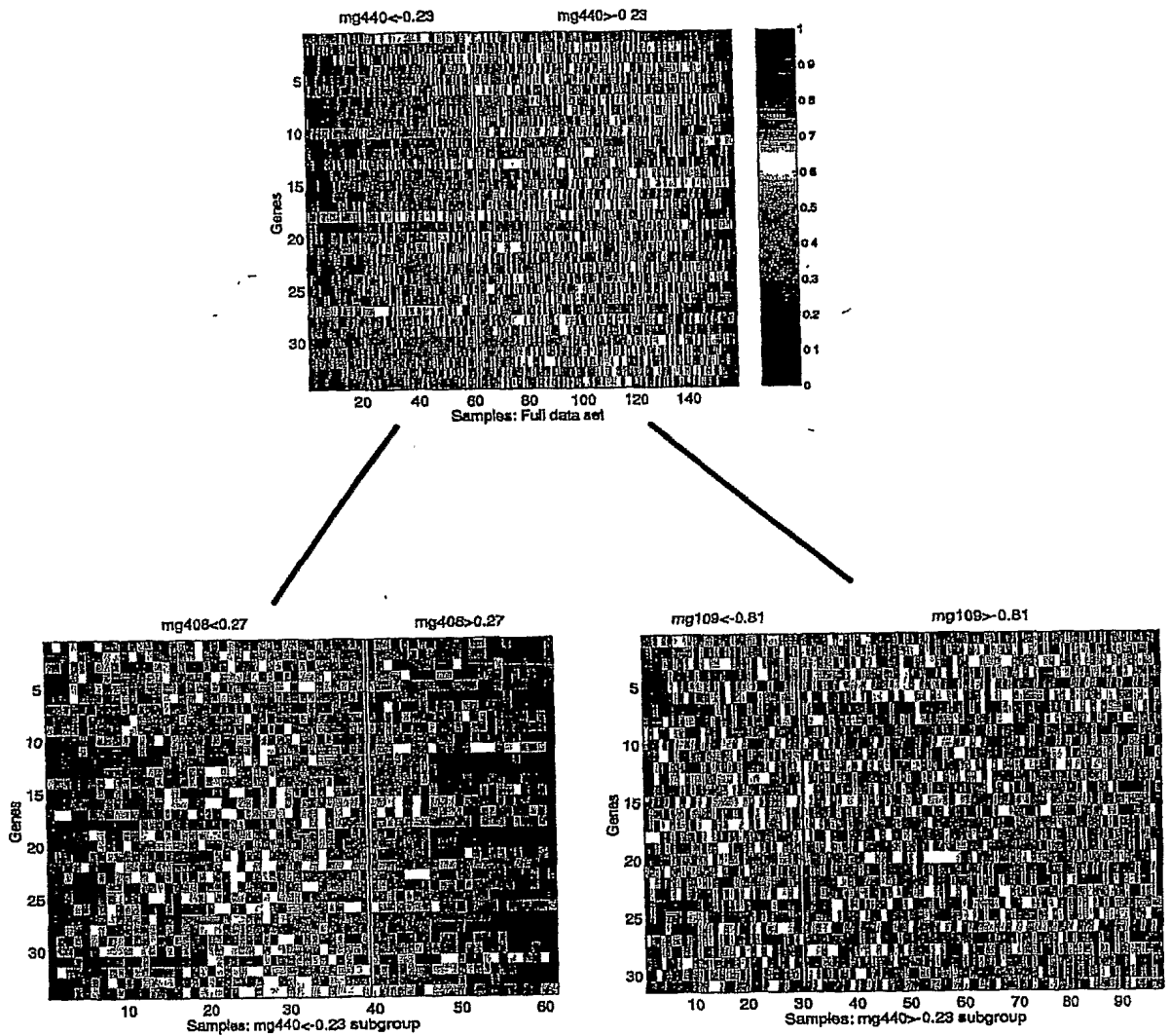
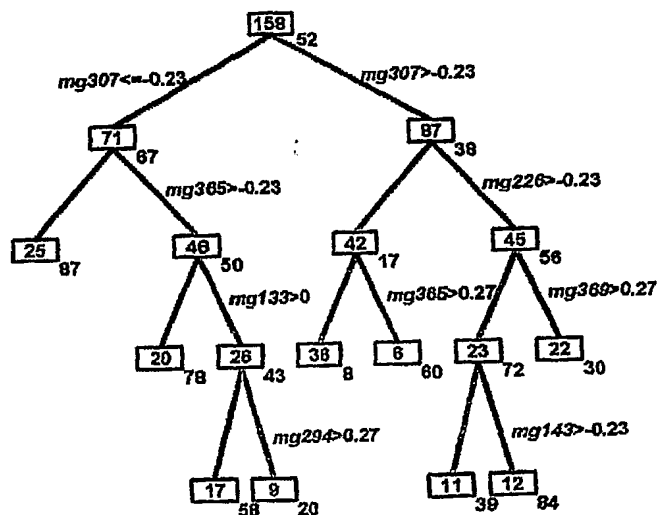
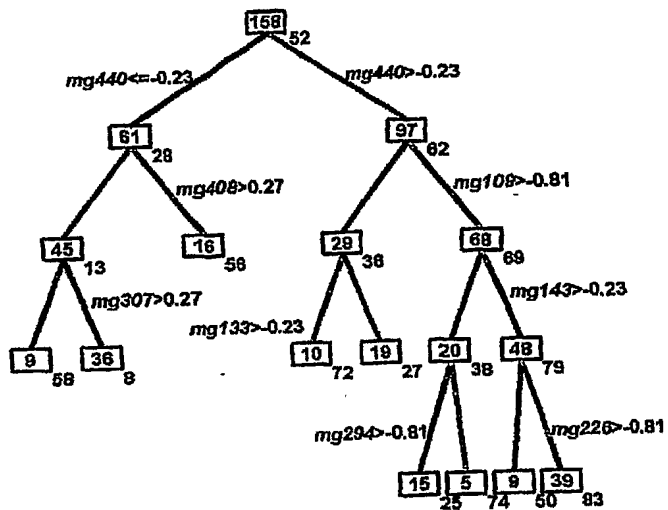
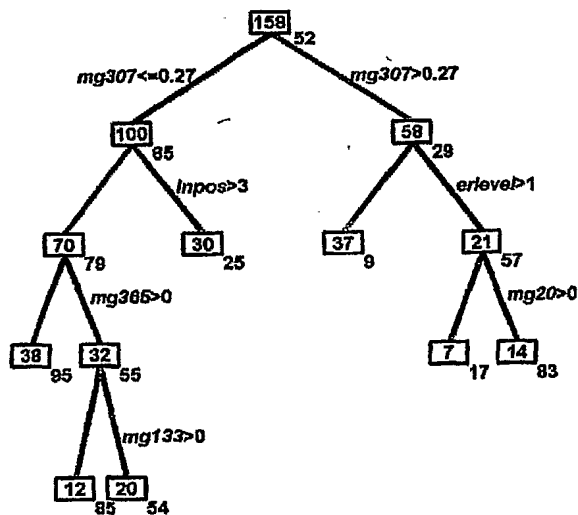
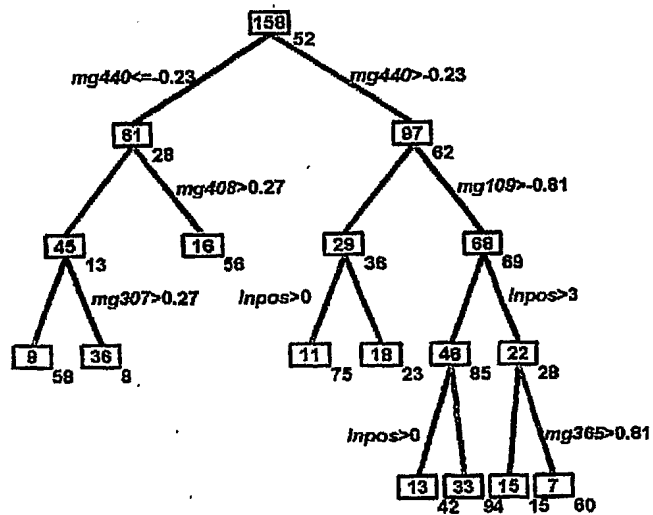


FIGURE 13

14
FIGURE 3(A)



14
FIGURE 8(B)



15
FIGURE 4(A)

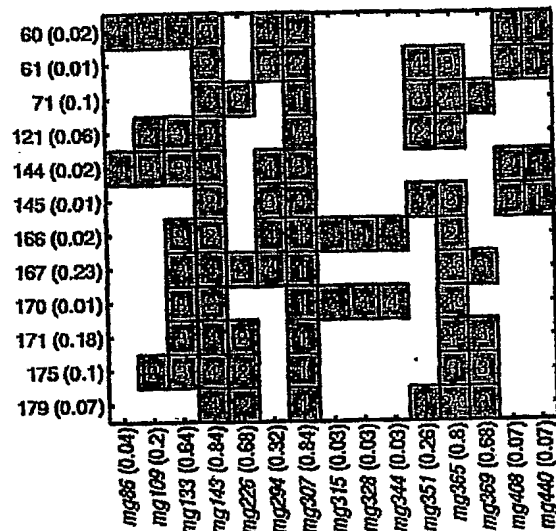
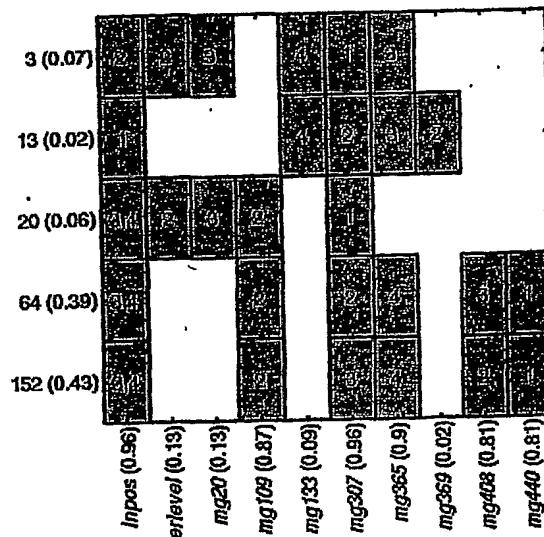


FIGURE 4(B)



160
FIGURE 5(A)

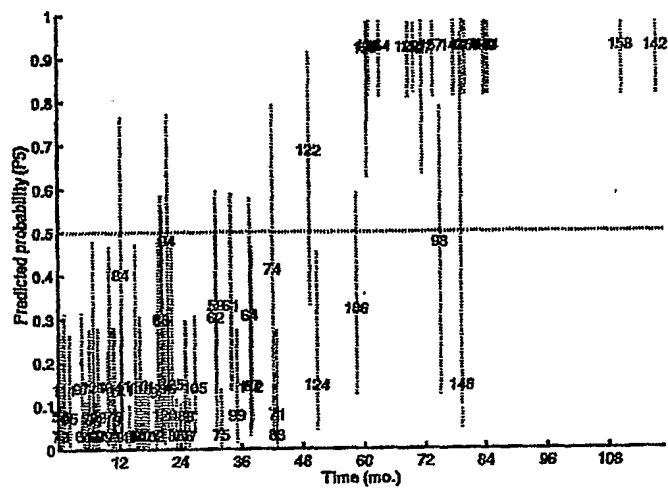


FIGURE 5(B)

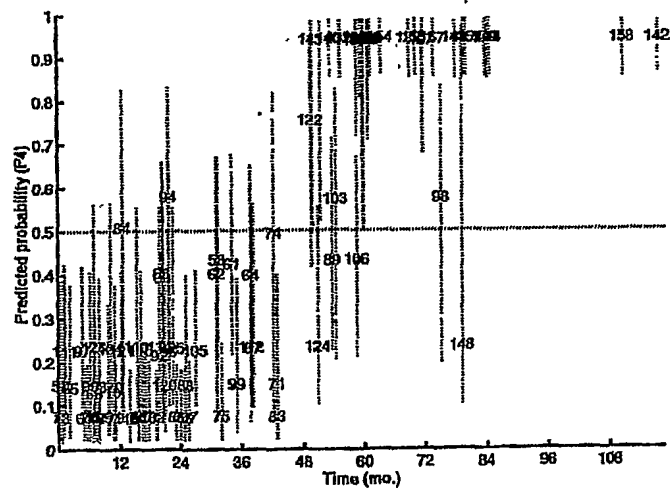


FIGURE 17

